

Sequence Listing

<110> Baker, Kevin P.
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone
Fong, Sherman
Gao, Wei-Qiang
Goddard, Audrey
Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth J.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Smith, Victoria
Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.

<120> Secreted and Transmembrane Polypeptides and Nucleic
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Cys Arg Asp Asp Ser Gly Thr Asp Asp Ser Val Asp Thr Gln Gln
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 cttctggatg tgaccgaccc agagaatgtc aagaggactg cccagtggtt 400

gaagaaccaa gttggggaga aaggctctg gggctgatc aataatgctg 450
gtgttcccg cgtgctggct cccactgact ggctgacact agaggactac 500
agagaaccta ttgaagtgaa cctgtttgga ctcatcagtg tgacactaaa 550
tatgcttcct ttggtaaga aagctcaagg gagagttatt aatgtctcca 600
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cagatccagt aaaggtaatt gaaaaaaaaac tcgcatttg ggagcagctg 800
tctccagaca tcaaacaaca atatggagaa gtttacattt aaaaaagtct 850
agacaaactg aaaggcaata aatcctatgt gaacatggac ctctctccgg 900
tggtagatgt catggaccac gctctaaca gtctcttccc taagactcat 950
tatgccgctg gaaaagatgc caaaattttc tggatacctc tgtctcacat 1000
gccagcagct ttgcaagact ttttattgtt gaaacagaaa gcagagctgg 1050
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aaaaaaaa 1508

<210> 10
<211> 319
<212> PRT
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 1-17
<223> Signal Peptide

<220>
<221> misc_feature

<222> 36-47, 108-113, 166-171, 198-203, 207-212
<223> N-myristoylation Sites.

<220>
<221> misc_feature
<222> 39-42
<223> Glycosaminoglycan Attachment Site.

<220>
<221> TRANSMEM
<222> 136-152
<223> Transmembrane Domain

<220>
<221> misc_feature
<222> 161-163, 187-190 and 253-256
<223> N-glycosylation Sites.

<400> 10
Met Leu Phe Trp Val Leu Gly Leu Leu Ile Leu Cys Gly Phe Leu
1 5 10 15
Trp Thr Arg Lys Gly Lys Leu Lys Ile Glu Asp Ile Thr Asp Lys
20 25 30
Tyr Ile Phe Ile Thr Gly Cys Asp Ser Gly Phe Gly Asn Leu Ala
35 40 45
Ala Arg Thr Phe Asp Lys Lys Gly Phe His Val Ile Ala Ala Cys
50 55 60
Leu Thr Glu Ser Gly Ser Thr Ala Leu Lys Ala Glu Thr Ser Glu
65 70 75
Arg Leu Arg Thr Val Leu Leu Asp Val Thr Asp Pro Glu Asn Val
80 85 90
Lys Arg Thr Ala Gln Trp Val Lys Asn Gln Val Gly Glu Lys Gly
95 100 105
Leu Trp Gly Leu Ile Asn Asn Ala Gly Val Pro Gly Val Leu Ala
110 115 120
Pro Thr Asp Trp Leu Thr Leu Glu Asp Tyr Arg Glu Pro Ile Glu
125 130 135
Val Asn Leu Phe Gly Leu Ile Ser Val Thr Leu Asn Met Leu Pro
140 145 150
Leu Val Lys Lys Ala Gln Gly Arg Val Ile Asn Val Ser Ser Val
155 160 165
Gly Gly Arg Leu Ala Ile Val Gly Gly Tyr Thr Pro Ser Lys
170 175 180
Tyr Ala Val Glu Gly Phe Asn Asp Ser Leu Arg Arg Asp Met Lys
185 190 195

Ala Phe Gly Val His Val Ser Cys Ile Glu Pro Gly Leu Phe Lys
 200 205 210
 Thr Asn Leu Ala Asp Pro Val Lys Val Ile Glu Lys Lys Leu Ala
 215 220 225
 Ile Trp Glu Gln Leu Ser Pro Asp Ile Lys Gln Gln Tyr Gly Glu
 230 235 240
 Gly Tyr Ile Glu Lys Ser Leu Asp Lys Leu Lys Gly Asn Lys Ser
 245 250 255
 Tyr Val Asn Met Asp Leu Ser Pro Val Val Glu Cys Met Asp His
 260 265 270
 Ala Leu Thr Ser Leu Phe Pro Lys Thr His Tyr Ala Ala Gly Lys
 275 280 285
 Asp Ala Lys Ile Phe Trp Ile Pro Leu Ser His Met Pro Ala Ala
 290 295 300
 Leu Gln Asp Phe Leu Leu Leu Lys Gln Lys Ala Glu Leu Ala Asn
 305 310 315
 Pro Lys Ala Val

<210> 11
 <211> 2720
 <212> DNA
 <213> Homo sapines

<400> 11
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 gccccttggg ccgtcgccac cactgttagtc atgtacccac cggccggcc 150
 gccgcctcat cgggacttca tctcggtgac gctgagctt ggcgagagct 200
 atgacaacag caagagttgg cggcggcgct cgtgctggag gaaatggaag 250
 caactgtcga gattgcagcg gaatatgatt ctcttccctcc ttgcctttct 300
 gctttctgt ggactcctct tctacatcaa cttggctgac cattggaaag 350
 ctctggcttt caggcttagag gaagagcaga agatgaggcc agaaattgct 400
 gggtaaaac cagcaaattcc acccgcttta ccagctcctc agaaggcgga 450
 caccgaccct gagaacttac ctgagatttc gtcacagaag acacaaagac 500
 acatccagcg gggaccaccc cacctgcaga ttagacccccc aagccaagac 550
 ctgaaggatg ggaccacccggaa ggaggccaca aaaaggcaag aagccccctgt 600
 ggatccccgc ccggaaggag atccgcagag gacagtcatc agctggaggg 650

gagcggtgat cgagcctgag cagggcaccg agctcccttc aagaagagca 700
gaagtgccca ccaaggctcc cctgccaccg gccaggacac agggcacacc 750
agtgcacatcg aactatcgcc agaagggcgt gattgacgac ttcctgcatg 800
catggaaagg ataccgcaag tttgcatgg gccatgacga gctgaaggct 850
gtgtccaggt cttcagtga gtgggttggc ctcggctctca cactgatcga 900
cgcgctggac accatgtgga tcttgggtct gaggaaagaa tttgaggaag 950
ccaggaagtg ggtgtcgaag aagttacact ttgaaaagga cgtggacgac 1000
aacctgtttg agagcacgat ccgcacatcctg ggggggctcc tgagtgccta 1050
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atcggttaat gcctgccttc agaacaccat ccaagattcc ttactcgat 1150
gtgaacatcg gtactggagt tgcccacccg ccacggtgga cctccgacag 1200
cactgtggcc gaggtgacca gcattcagct ggagttccgg gagctctccc 1250
gtctcacagg ggataagaag tttcaggagg cagtggagaa ggtgacacag 1300
cacatccacg gcctgtctgg gaagaaggat gggctggtgc ccatgttcat 1350
caatacccac agtggcctct tcacccacccct gggcgtattc acgctggcg 1400
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tcctggggga gacgctcaag tatctgttct tgctttctc ccatgaccca 2050
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ttgatttgct ctaaccgcaa 2720

<210> 12
<211> 699
<212> PRT
<213> Homo sapiens

<220>
<221> TRANSMEM
<222> 21-40 and 84-105
<223> Transmembrane Domain (type II)

<400> 12
Met Ala Ala Cys Glu Gly Arg Arg Ser Gly Ala Leu Gly Ser Ser
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Gln Ser Asp Phe Leu Thr Pro Pro Val Gly Gly Ala Pro Trp Ala
20 25 30
Val Ala Thr Thr Val Val Met Tyr Pro Pro Pro Pro Pro Pro Pro
35 40 45
His Arg Asp Phe Ile Ser Val Thr Leu Ser Phe Gly Glu Ser Tyr
50 55 60
Asp Asn Ser Lys Ser Trp Arg Arg Arg Ser Cys Trp Arg Lys Trp
65 70 75
Lys Gln Leu Ser Arg Leu Gln Arg Asn Met Ile Leu Phe Leu Leu
80 85 90
Ala Phe Leu Leu Phe Cys Gly Leu Leu Phe Tyr Ile Asn Leu Ala
95 100 105

Asp His Trp Lys Ala Leu Ala Phe Arg Leu Glu Glu Glu Gln Lys
 110 115 120
 Met Arg Pro Glu Ile Ala Gly Leu Lys Pro Ala Asn Pro Pro Val
 125 130 135
 Leu Pro Ala Pro Gln Lys Ala Asp Thr Asp Pro Glu Asn Leu Pro
 140 145 150
 Glu Ile Ser Ser Gln Lys Thr Gln Arg His Ile Gln Arg Gly Pro
 155 160 165
 Pro His Leu Gln Ile Arg Pro Pro Ser Gln Asp Leu Lys Asp Gly
 170 175 180
 Thr Gln Glu Glu Ala Thr Lys Arg Gln Glu Ala Pro Val Asp Pro
 185 190 195
 Arg Pro Glu Gly Asp Pro Gln Arg Thr Val Ile Ser Trp Arg Gly
 200 205 210
 Ala Val Ile Glu Pro Glu Gln Gly Thr Glu Leu Pro Ser Arg Arg
 215 220 225
 Ala Glu Val Pro Thr Lys Pro Pro Leu Pro Pro Ala Arg Thr Gln
 230 235 240
 Gly Thr Pro Val His Leu Asn Tyr Arg Gln Lys Gly Val Ile Asp
 245 250 255
 Val Phe Leu His Ala Trp Lys Gly Tyr Arg Lys Phe Ala Trp Gly
 260 265 270
 His Asp Glu Leu Lys Pro Val Ser Arg Ser Phe Ser Glu Trp Phe
 275 280 285
 Gly Leu Gly Leu Thr Leu Ile Asp Ala Leu Asp Thr Met Trp Ile
 290 295 300
 Leu Gly Leu Arg Lys Glu Phe Glu Glu Ala Arg Lys Trp Val Ser
 305 310 315
 Lys Lys Leu His Phe Glu Lys Asp Val Asp Val Asn Leu Phe Glu
 320 325 330
 Ser Thr Ile Arg Ile Leu Gly Gly Leu Leu Ser Ala Tyr His Leu
 335 340 345
 Ser Gly Asp Ser Leu Phe Leu Arg Lys Ala Glu Asp Phe Gly Asn
 350 355 360
 Arg Leu Met Pro Ala Phe Arg Thr Pro Ser Lys Ile Pro Tyr Ser
 365 370 375
 Asp Val Asn Ile Gly Thr Gly Val Ala His Pro Pro Arg Trp Thr
 380 385 390
 Ser Asp Ser Thr Val Ala Glu Val Thr Ser Ile Gln Leu Glu Phe

395	400	405
Arg Glu Leu Ser Arg Leu Thr Gly Asp	Lys Lys Phe Gln Glu Ala	
410	415	420
Val Glu Lys Val Thr Gln His Ile His	Gly Leu Ser Gly Lys Lys	
425	430	435
Asp Gly Leu Val Pro Met Phe Ile Asn	Thr His Ser Gly Leu Phe	
440	445	450
Thr His Leu Gly Val Phe Thr Leu Gly	Ala Arg Ala Asp Ser Tyr	
455	460	465
Tyr Glu Tyr Leu Leu Lys Gln Trp Ile	Gln Gly Gly Lys Gln Glu	
470	475	480
Thr Gln Leu Leu Glu Asp Tyr Val Glu	Ala Ile Glu Gly Val Arg	
485	490	495
Thr His Leu Leu Arg His Ser Glu Pro	Ser Lys Leu Thr Phe Val	
500	505	510
Gly Glu Leu Ala His Gly Arg Phe Ser	Ala Lys Met Asp His Leu	
515	520	525
Val Cys Phe Leu Pro Gly Thr Leu Ala	Leu Gly Val Tyr His Gly	
530	535	540
Leu Pro Ala Ser His Met Glu Leu Ala	Gln Glu Leu Met Glu Thr	
545	550	555
Cys Tyr Gln Met Asn Arg Gln Met Glu	Thr Gly Leu Ser Pro Glu	
560	565	570
Ile Val His Phe Asn Leu Tyr Pro Gln	Pro Gly Arg Arg Asp Val	
575	580	585
Glu Val Lys Pro Ala Asp Arg His Asn	Leu Leu Arg Pro Glu Thr	
590	595	600
Val Glu Ser Leu Phe Tyr Leu Tyr Arg	Val Thr Gly Asp Arg Lys	
605	610	615
Tyr Gln Asp Trp Gly Trp Glu Ile Leu	Gln Ser Phe Ser Arg Phe	
620	625	630
Thr Arg Val Pro Ser Gly Gly Tyr Ser	Ser Ile Asn Asn Val Gln	
635	640	645
Asp Pro Gln Lys Pro Glu Pro Arg Asp	Lys Met Glu Ser Phe Phe	
650	655	660
Leu Gly Glu Thr Leu Lys Tyr Leu Phe	Leu Leu Phe Ser Asp Asp	
665	670	675
Pro Asn Leu Leu Ser Leu Asp Ala Tyr	Val Phe Asn Thr Glu Ala	
680	685	690

His Pro Leu Pro Ile Trp Thr Pro Ala
695

<210> 13
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 13
cgccagaagg gcgtgattga cgtc 24

<210> 14
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 14
ccatccttct tcccagacag gccg 24

<210> 15
<211> 44
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-44
<223> Synthetic construct.

<400> 15
gaagcctgtg tccaggtcct tcagtgagtg gtttggcctc ggtc 44

<210> 16
<211> 1524
<212> DNA
<213> Homo sapiens

<400> 16
ggcgccgcgt aggccccggga ggccgggccc gcccggctgc gagcgcctgc 50
cccatgcgcc gccgcctctc cgcacgatgt tcccctcgcg gagaaagcg 100
ggcgcagctgc cctgggagga cggcaggtcc ggggtgcctc ccggcggcct 150
ccctcggaag tggccgtct tccacctgtt cgtggcctgc ctctcgctgg 200
gcttcttctc cctactctgg ctgcagctca gctgctctgg ggacgtggcc 250

cgggcagtca ggggacaagg gcaggagacc tcggccctc cccgtgcctg 300
ccccccagag cgcgcgcctg agcaactggga agaagacgca tcctggggcc 350
cccaccgcct ggcagtgctg gtgcgccttc gcgaacgcct cgaggagctc 400
ctggtcttcg tgccccacat gcgcgccttc ctgagcagga agaagatccg 450
gcaccacatc tacgtgctca accaggtgga ccacttcagg ttcaaccggg 500
cagcgctcat caacgtggc ttcctggaga gcagcaacag cacggactac 550
attgccatgc acgacggttga cctgctccct ctcaacgagg agctggacta 600
tggcttcctt gaggctggc cttccacgt ggcctccccc gagctccacc 650
ctctctacca ctacaagacc tatgtcggcg gcacccctgct gctctccaag 700
cagcaactacc ggctgtgcaa tggatgtcc aaccgcttct gggctgggg 750
ccgcgaggac gacgagttct accggcgcat taaggagct gggctccagc 800
tttccgccc ctggaaatc acaactgggt acaagacatt tcgcccaccc 850
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acaggagcag ttcaaggtgg acagggaggg aggcctgaac actgtgaagt 950
accatgtggc ttccgcact gcctgtctg tggcgggc cccctgcact 1000
gtcctaaca tcatgttga ctgtgacaag accgcccacac cctggcgcac 1050
attcagctga gctggatgga cagtgaggaa gcctgtaccc acaggccata 1100
ttgctcaggc tcaggacaag gcctcaggtc gtggcccgag ctctgacagg 1150
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tgaacaggac aacctctcat caccccaaaa aaaaaaaaaa aaaaaaaaaa 1500
aaaaaaaaaa aaaaaaaaaa aaaa 1524

<210> 17
<211> 327
<212> PRT
<213> Homo sapiens

<220>

<221> sig_peptide
 <222> 1-42
 <223> Signal peptide.

<220>
 <221> misc_feature
 <222> 19-25, 65-71, 247-253, 285-291, 303-310
 <223> N-myristoylation site.

<220>
 <221> misc_feature
 <222> 27-31
 <223> cAMP- and cGMP-dependent protein kinase phosphorylation site.

<220>
 <221> TRANSMEM
 <222> 29-49
 <223> Transmembrane domain (type II).

<220>
 <221> misc_feature
 <222> 154-158
 <223> N-glycosylation site.

<220>
 <221> misc_feature
 <222> 226-233
 <223> Tyrosine kinase phosphorylation site.

<400> 17

Met	Phe	Pro	Ser	Arg	Arg	Lys	Ala	Ala	Gln	Leu	Pro	Trp	Glu	Asp
1				5				10					15	

Gly	Arg	Ser	Gly	Leu	Leu	Ser	Gly	Gly	Leu	Pro	Arg	Lys	Cys	Ser
				20				25					30	

Val	Phe	His	Leu	Phe	Val	Ala	Cys	Leu	Ser	Leu	Gly	Phe	Phe	Ser
				35				40					45	

Leu	Leu	Trp	Leu	Gln	Leu	Ser	Cys	Ser	Gly	Asp	Val	Ala	Arg	Ala
				50				55					60	

Val	Arg	Gly	Gln	Gly	Gln	Glu	Thr	Ser	Gly	Pro	Pro	Arg	Ala	Cys
				65				70					75	

Pro	Pro	Glu	Pro	Pro	Glu	His	Trp	Glu	Glu	Asp	Ala	Ser	Trp	
				80				85					90	

Gly	Pro	His	Arg	Leu	Ala	Val	Leu	Val	Pro	Phe	Arg	Glu	Arg	Phe
				95				100					105	

Glu	Glu	Leu	Leu	Val	Phe	Val	Pro	His	Met	Arg	Arg	Phe	Leu	Ser
				110				115					120	

Arg	Lys	Lys	Ile	Arg	His	His	Ile	Tyr	Val	Leu	Asn	Gln	Val	Asp
				125				130					135	

His Phe Arg Phe Asn Arg Ala Ala Leu Ile Asn Val Gly Phe Leu

140	145	150
Glu Ser Ser Asn Ser Thr Asp Tyr Ile Ala Met His Asp Val Asp		
155	160	165
Leu Leu Pro Leu Asn Glu Glu Leu Asp Tyr Gly Phe Pro Glu Ala		
170	175	180
Gly Pro Phe His Val Ala Ser Pro Glu Leu His Pro Leu Tyr His		
185	190	195
Tyr Lys Thr Tyr Val Gly Gly Ile Leu Leu Leu Ser Lys Gln His		
200	205	210
Tyr Arg Leu Cys Asn Gly Met Ser Asn Arg Phe Trp Gly Trp Gly		
215	220	225
Arg Glu Asp Asp Glu Phe Tyr Arg Arg Ile Lys Gly Ala Gly Leu		
230	235	240
Gln Leu Phe Arg Pro Ser Gly Ile Thr Thr Gly Tyr Lys Thr Phe		
245	250	255
Arg His Leu His Asp Pro Ala Trp Arg Lys Arg Asp Gln Lys Arg		
260	265	270
Ile Ala Ala Gln Lys Gln Glu Gln Phe Lys Val Asp Arg Glu Gly		
275	280	285
Gly Leu Asn Thr Val Lys Tyr His Val Ala Ser Arg Thr Ala Leu		
290	295	300
Ser Val Gly Gly Ala Pro Cys Thr Val Leu Asn Ile Met Leu Asp		
305	310	315
Cys Asp Lys Thr Ala Thr Pro Trp Cys Thr Phe Ser		
320	325	

<210> 18
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 18
gcgaacgctt cgaggagtcc tgg 23

<210> 19
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence

<222> 1-24
<223> Synthetic construct

<400> 19
gcagtgcggg aagccacatg gtac 24

<210> 20
<211> 46
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-46
<223> Synthetic construct.

<400> 20
cttcctgagc aggaagaaga tccggcacca catctacgtg ctcaac 46

<210> 21
<211> 494
<212> DNA
<213> Homo sapiens

<400> 21
caatgtttgc ctatccacct ccccaagcc ccttaccta tgctgctgct 50
aacgctgctg ctgctgctgc tgctgcttaa aggctcatgc ttggagtggg 100
gactggtcgg tgcccagaaa gtctcttctg ccactgacgc ccccatcagg 150
gattgggcct tctttccccc ttccttctg tgtctcctgc ctcatcggcc 200
tgccatgacc tgcagccaag cccagcccg tgggaaggg gagaaagtgg 250
ggatggcta agaaagctgg gagataggg acaagaagagg gtagtgggtg 300
ggctaggggg gctgccttat ttaaagtggt tgtttatgat tcttatacta 350
atttatacaa agatattaag gcccgttca ttaagaaatt gttcccttcc 400
cctgtgttca atgttgtaa agattgttct gtgtaaatat gtcttataaa 450
taaacagttt aaagctgaaa aaaaaaaaaa aaaaaaaaaa aaaa 494

<210> 22
<211> 73
<212> PRT
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 1-15
<223> Signal peptide.

<220>
<221> misc_feature
<222> 3-18

<223> Growth factor and cytokines receptors family.
 <400> 22
 Met Leu Leu Leu Thr Leu Leu Leu Leu Leu Leu Lys Gly
 1 5 10 15
 Ser Cys Leu Glu Trp Gly Leu Val Gly Ala Gln Lys Val Ser Ser
 20 25 30
 Ala Thr Asp Ala Pro Ile Arg Asp Trp Ala Phe Phe Pro Pro Ser
 35 40 45
 Phe Leu Cys Leu Leu Pro His Arg Pro Ala Met Thr Cys Ser Gln
 50 55 60
 Ala Gln Pro Arg Gly Glu Gly Glu Lys Val Gly Asp Gly
 65 70

<210> 23
 <211> 2883
 <212> DNA
 <213> Homo sapiens

<400> 23
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 cagcggacaa aggagcatgt ccgcgcggg gaaggccgt cctccggccg 100
 ccataaggct ccggtcgccc ctgggcccgc gccgcgtcc tgcccgcccc 150
 ggctccgggg cggcccgcta ggccagtgcg ccgcccgtcg ccccgccaggc 200
 cccggcccgc agcatggagc caccggacg ccggcggggc cgcgcgcagc 250
 cggcgctgtt gtcgcgcgtc tcgctgttag cgctgctcgc gtcgtggga 300
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 tggtgtgcag cagcctggaa ctgcgcagg tcctgcccc agatactctg 450
 cccaaccgca cggtcaccct gattctgagt aacaataaga tatccgagct 500
 gaagaatggc tcattttctg ggttaagtct cttgaaaga ttggacctcc 550
 gaaacaatct tatttagtagt atagatccag gtgcctctg gggactgtca 600
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 cggctttgg aattccagac tgagtatct ttgtgtgact gtaacataact 800
 gtggatgcat cgctggtaa aggagaagaa catcacggta cgggataccca 850

ggtgtgttta tcctaagtca ctgcaggccc aaccagtac aaggcgtgaag 900
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<210> 24
<211> 616
<212> PRT
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 1-33
<223> Signal peptide.

<220>
<221> TRANSMEM
<222> 13-40
<223> Transmembrane domain (type II).

<400> 24
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35 40 45
Asp Gly Arg Pro Arg Gly Ala Gly Arg Ala Ala Gly Ala Ala Glu
50 55 60
Gly Lys Val Val Cys Ser Ser Leu Glu Leu Ala Gln Val Leu Pro
65 70 75
Pro Asp Thr Leu Pro Asn Arg Thr Val Thr Leu Ile Leu Ser Asn
80 85 90

Asn Lys Ile Ser Glu Leu Lys Asn Gly Ser Phe Ser Gly Leu Ser
 95 100 105
 Leu Leu Glu Arg Leu Asp Leu Arg Asn Asn Leu Ile Ser Ser Ile
 110 115 120
 Asp Pro Gly Ala Phe Trp Gly Leu Ser Ser Leu Lys Arg Leu Asp
 125 130 135
 Leu Thr Asn Asn Arg Ile Gly Cys Leu Asn Ala Asp Ile Phe Arg
 140 145 150
 Gly Leu Thr Asn Leu Val Arg Leu Asn Leu Ser Gly Asn Leu Phe
 155 160 165
 Ser Ser Leu Ser Gln Gly Thr Phe Asp Tyr Leu Ala Ser Leu Arg
 170 175 180
 Ser Leu Glu Phe Gln Thr Glu Tyr Leu Leu Cys Asp Cys Asn Ile
 185 190 195
 Leu Trp Met His Arg Trp Val Lys Glu Lys Asn Ile Thr Val Arg
 200 205 210
 Asp Thr Arg Cys Val Tyr Pro Lys Ser Leu Gln Ala Gln Pro Val
 215 220 225
 Thr Gly Val Lys Gln Glu Leu Leu Thr Cys Asp Pro Pro Leu Glu
 230 235 240
 Leu Pro Ser Phe Tyr Met Thr Pro Ser His Arg Gln Val Val Phe
 245 250 255
 Glu Gly Asp Ser Leu Pro Phe Gln Cys Met Ala Ser Tyr Ile Asp
 260 265 270
 Gln Asp Met Gln Val Leu Trp Tyr Gln Asp Gly Arg Ile Val Glu
 275 280 285
 Thr Asp Glu Ser Gln Gly Ile Phe Val Glu Lys Asn Met Ile His
 290 295 300
 Asn Cys Ser Leu Ile Ala Ser Ala Leu Thr Ile Ser Asn Ile Gln
 305 310 315
 Ala Gly Ser Thr Gly Asn Trp Gly Cys His Val Gln Thr Lys Arg
 320 325 330
 Gly Asn Asn Thr Arg Thr Val Asp Ile Val Val Leu Glu Ser Ser
 335 340 345
 Ala Gln Tyr Cys Pro Pro Glu Arg Val Val Asn Asn Lys Gly Asp
 350 355 360
 Phe Arg Trp Pro Arg Thr Leu Ala Gly Ile Thr Ala Tyr Leu Gln
 365 370 375
 Cys Thr Arg Asn Thr His Gly Ser Gly Ile Tyr Pro Gly Asn Pro

380	385	390
Gln Asp Glu Arg Lys Ala Trp Arg Arg	Cys Asp Arg Gly Gly	Phe
395	400	405
Trp Ala Asp Asp Asp Tyr Ser Arg Cys	Gln Tyr Ala Asn Asp Val	
410	415	420
Thr Arg Val Leu Tyr Met Phe Asn Gln	Met Pro Leu Asn Leu Thr	
425	430	435
Asn Ala Val Ala Thr Ala Arg Gln Leu	Leu Ala Tyr Thr Val Glu	
440	445	450
Ala Ala Asn Phe Ser Asp Lys Met Asp Val	Ile Phe Val Ala Glu	
455	460	465
Met Ile Glu Lys Phe Gly Arg Phe Thr	Lys Glu Glu Lys Ser Lys	
470	475	480
Glu Leu Gly Asp Val Met Val Asp Ile Ala	Ser Asn Ile Met Leu	
485	490	495
Ala Asp Glu Arg Val Leu Trp Leu Ala	Gln Arg Glu Ala Lys Ala	
500	505	510
Cys Ser Arg Ile Val Gln Cys Leu Gln	Arg Ile Ala Thr Tyr Arg	
515	520	525
Leu Ala Gly Gly Ala His Val Tyr Ser	Thr Tyr Ser Pro Asn Ile	
530	535	540
Ala Leu Glu Ala Tyr Val Ile Lys Ser	Thr Gly Phe Thr Gly Met	
545	550	555
Thr Cys Thr Val Phe Gln Lys Val Ala	Ala Ser Asp Arg Thr Gly	
560	565	570
Leu Ser Asp Tyr Gly Arg Arg Asp Pro	Glu Gly Asn Leu Asp Lys	
575	580	585
Gln Leu Ser Phe Lys Cys Asn Val Ser	Asn Thr Phe Ser Ser Leu	
590	595	600
Ala Leu Lys Val Cys Tyr Ile Leu Gln	Ser Phe Lys Thr Ile Tyr	
605	610	615
Ser		

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 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24

<223> Synthetic construct

<400> 25

gaggactcac caatctgggtt cggc 24

<210> 26

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 26

aactggaaag gaaggctgtc tccc 24

<210> 27

<211> 50

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-50

<223> Synthetic construct.

<400> 27

gtaaaggaga agaacatcac ggtacggat accaggtgtg tttatcctaa 50

<210> 28

<211> 683

<212> DNA

<213> Homo sapiens

<400> 28

gcgtggggat gtctaggagc tcgaagggtgg tgctgggcct ctcggtgctg 50

ctgacggcgg ccacagtggc cggcgtacat gtgaagcagc agtgggacca 100

gcagaggctt cgtgacggag ttatcagaga cattgagagg caaattcgg 150

aaaaagaaaa cattcgtctt ttgggagaac agattatttt gactgagcaa 200

cttgaagcag aaagagagaa gatgttattt gcaaaaggat ctcaaaaatc 250

atgacttgaa tgtgaaatat ctgttggaca gacaacacga gtttgtgtgt 300

gtgtgttgc ggagagtagc ttagtagtat cttcatctt tttttggtc 350

actgtccttt taaacttgat caaataaagg acagtgggtc atataagtta 400

ctgctttcag ggtcccttat atctgaataa aggagtgtgg gcagacactt 450

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tgtccagtgc ttagggttgt tactgagaag cactgccgag cttgtgagaa 550

ggaaggggatg gatagtagca tccacacctgag tagtctgatc agtcggcatg 600
atgacgaagc cacgagaaca tcgacacctgag aaggactgga ggaagggtgaa 650
gtggagggag agacgctcct gatcgtcga tcc 683

<210> 29
<211> 81
<212> PRT
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 1-21
<223> Signal peptide.

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Thr Ala Ala Thr Val Ala Gly Val His Val Lys Gln Gln Trp Asp
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Gln Gln Arg Leu Arg Asp Gly Val Ile Arg Asp Ile Glu Arg Gln
35 40 45
Ile Arg Lys Lys Glu Asn Ile Arg Leu Leu Gly Glu Gln Ile Ile
50 55 60
Leu Thr Glu Gln Leu Glu Ala Glu Arg Glu Lys Met Leu Leu Ala
65 70 75
Lys Gly Ser Gln Lys Ser
80

<210> 30
<211> 2128
<212> DNA
<213> Homo sapiens

<400> 30
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tccgtggatt cctctgctaa gaccgctgcc atgccagtga cggtaacccg 150
caccaccatc acaaccacca cgacgtcata ttcgggcctg gggccccca 200
tgatcgtggg gtcccccctcg gcccgtacac agccccctggg tctccttcgc 250
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tctgcttctc cgtgaccctg atcatcctca tcgtggagct gtgcgggctc 400
caggccccgtc tccccctgtc ttggcgcaac ttccccatca ctttcgcctg 450

ctatgcggcc ctcttctgcc tctcgccctc catcatctac cccaccacct 500
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cccaactatt ctctgtggta tgaaaaag 2128

<210> 31
<211> 322
<212> PRT
<213> Homo sapiens

<400> 31
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Ala Leu Thr Gln Pro Leu Gly Leu Leu Arg Leu Leu Gln Leu Val
35 40 45
Ser Thr Cys Val Ala Phe Ser Leu Val Ala Ser Val Gly Ala Trp
50 55 60
Thr Gly Ser Met Gly Asn Trp Ser Met Phe Thr Trp Cys Phe Cys
65 70 75
Phe Ser Val Thr Leu Ile Ile Leu Ile Val Glu Leu Cys Gly Leu
80 85 90
Gln Ala Arg Phe Pro Leu Ser Trp Arg Asn Phe Pro Ile Thr Phe
95 100 105
Ala Cys Tyr Ala Ala Leu Phe Cys Leu Ser Ala Ser Ile Ile Tyr
110 115 120
Pro Thr Thr Tyr Val Gln Phe Leu Ser His Gly Arg Ser Arg Asp
125 130 135
His Ala Ile Ala Ala Thr Phe Phe Ser Cys Ile Ala Cys Val Ala
140 145 150
Tyr Ala Thr Glu Val Ala Trp Thr Arg Ala Arg Pro Gly Glu Ile
155 160 165
Thr Gly Tyr Met Ala Thr Val Pro Gly Leu Leu Lys Val Leu Glu
170 175 180
Thr Phe Val Ala Cys Ile Ile Phe Ala Phe Ile Ser Asp Pro Asn
185 190 195
Leu Tyr Gln His Gln Pro Ala Leu Glu Trp Cys Val Ala Val Tyr
200 205 210

Ala Ile Cys Phe Ile Leu Ala Ala Ile Ala Ile Leu Leu Asn Leu
215 220 225
Gly Glu Cys Thr Asn Val Leu Pro Ile Pro Phe Pro Ser Phe Leu
230 235 240
Ser Gly Leu Ala Leu Leu Ser Val Leu Leu Tyr Ala Thr Ala Leu
245 250 255
Val Leu Trp Pro Leu Tyr Gln Phe Asp Glu Lys Tyr Gly Gly Gln
260 265 270
Pro Arg Arg Ser Arg Asp Val Ser Cys Ser Arg Ser His Ala Tyr
275 280 285
Tyr Val Cys Ala Trp Asp Arg Arg Leu Ala Val Ala Ile Leu Thr
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Ala Ile Asn Leu Leu Ala Tyr Val Ala Asp Leu Val His Ser Ala
305 310 315
His Leu Val Phe Val Lys Val
320

<210> 32
<211> 3680
<212> DNA
<213> Homo sapiens

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ctggccagcc tatgcatttt taagaaattha ttctgtatta ggtgctgtgc 200
taaacattgg qcactacagt gacaaaaca gactgaattc cccaagagcc 250
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 <400> 33
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 1 5 10 15
 Phe Gly Thr Val Ser Cys Glu Tyr Met Leu Gly Ser Pro Leu Ser
 20 25 30
 Ser Leu Ala Gln Val Asn Leu Ser Pro Phe Ser His Pro Lys Val
 35 40 45
 His Met Asp Pro Asn Tyr Cys His Pro Ser Thr Ser Leu His Leu
 50 55 60
 Cys Ser Leu Ala Trp Ser Phe Thr Arg Leu Leu His Pro Pro Leu
 65 70 75
 Ser Pro Gly Ile Ser Gln Val Val Lys Asp His Val Thr Lys Pro
 80 85 90
 Thr Ala Met Ala Gln Gly Arg Val Ala His Leu Ile Glu Trp Lys
 95 100 105
 Gly Trp Ser Lys Pro Ser Asp Ser Pro Ala Ala Leu Glu Ser Ala
 110 115 120
 Phe Ser Ser Tyr Ser Asp Leu Ser Glu Gly Glu Gln Glu Ala Arg
 125 130 135
 Phe Ala Ala Gly Val Ala Glu Gln Phe Ala Ile Ala Glu Ala Lys
 140 145 150
 Leu Arg Ala Trp Ser Ser Val Asp Gly Glu Asp Ser Thr Asp Asp
 155 160 165
 Ser Tyr Asp Glu Asp Phe Ala Gly Gly Met Asp Thr Asp Met Ala
 170 175 180
 Gly Gln Leu Pro Leu Gly Pro His Leu Gln Asp Leu Phe Thr Gly
 185 190 195
 His Arg Phe Ser Arg Pro Val Arg Gln Gly Ser Val Glu Pro Glu
 200 205 210
 Ser Asp Cys Ser Gln Thr Val Ser Pro Asp Thr Leu Cys Ser Ser
 215 220 225
 Leu Cys Ser Leu Glu Asp Gly Leu Leu Gly Ser Pro Ala Arg Leu
 230 235 240

Ala Ser Gln Leu Leu Gly Asp Glu Leu Leu Leu Ala Lys Leu Pro
 245 250 255

Pro Ser Arg Glu Ser Ala Phe Arg Ser Leu Gly Pro Leu Glu Ala
 260 265 270

Gln Asp Ser Leu Tyr Asn Ser Pro Leu Thr Glu Ser Cys Leu Ser
 275 280 285

Pro Ala Glu Glu Glu Pro Ala Pro Cys Lys Asp Cys Gln Pro Leu
 290 295 300

Cys Pro Pro Leu Thr Gly Ser Trp Glu Arg Gln Arg Gln Ala Ser
 305 310 315

Asp Leu Ala Ser Ser Gly Val Val Ser Leu Asp Glu Asp Glu Ala
 320 325 330

Glu Pro Glu Glu Gln
 335

<210> 34
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-25
 <223> Synthetic construct

<400> 34
 tgtcctttgt cccagacttc tgtcc 25

<210> 35
 <211> 50
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-50
 <223> Synthetic construct.

<400> 35
 ctggatgcta atgtgtccag taaatgatcc ccttatcccg tcgcgatgct 50

<210> 36
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 36

ttccactcaa tgaggtgagc cactc 25

<210> 37
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-23
<223> Synthetic construct.

<400> 37
ggcgagccct aactatccag gag 23

<210> 38
<211> 39
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-39
<223> Synthetic construct.

<400> 38
ggagatcgct gcgctggcca ggtcctccct gcatggtat 39

<210> 39
<211> 22
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-22
<223> Synthetic construct.

<400> 39
ctgctgcaaa gcgagccctct tg 22

<210> 40
<211> 2084
<212> DNA
<213> Homo sapiens

<400> 40
ggtcctggg cgctctgtta cacaaggcaag atacagccag ccccacctaa 50
ttttgttcc ctggcacccct cctgctcagt ggcacattgt cacacttaac 100
ccatctgttt tctctaattgc acgacagatt cctttcagac aggacaactg 150
tgcattttca gttcctgatt gtaaatacct cctaagcctg aagcttctgt 200
tactagccat tgtgagcttc agtttcttca tctgcaaaat gggcataata 250
caatctattc ttgccacatc aaggattgt tattccctta aaaaaaaaaacc 300

aataccaaag aagcctacaa tgttggcctt agccaaaatt ctgttgattt 350
caacgttgtt ttattcactt ctatcgggaa gccatggaaa agaaaatcaa 400
gacataaaaca caacacagaa cattgcagaa gttttaaaaa caatggaaaa 450
taaacctatt tctttggaaa gtgaagcaaa cttaaactca gataaagaaa 500
atataaaccac ctcaaattctc aaggcgagtc attccctcc tttgaatcta 550
cccaacaaca gccacggaat aacagattc tccagtaact catcagcaga 600
gcattcttg ggcagtctaa aacccacatc taccattcc acaagccctc 650
ccttgatcca tagcttgtt tctaaagtgc cttggaatgc acctatagca 700
gatgaagatc ttttgcctat ctcagcacat cccaatgcta cacctgctct 750
gtcttcagaa aacttcactt ggtcttggt caatgacacc gtgaaaactc 800
ctgataacag ttccattaca gttagcatcc tctcttcaga accaacttct 850
ccatctgtga cccccttgat agtggAACCA agtggatggc ttaccacaaa 900
cagtgatagc ttcactgggt ttaccctta tcaagaaaaa acaactctac 950
agcctacctt aaaattcacc aataattcaa aactcttcc aaatacgtca 1000
gatccccaaa aagaaaaatag aaatacagga atagtattcg gggccatttt 1050
aggtgctatt ctgggtgtct cattgcttac tcttggcacttggc tacttggtt 1100
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agaaatgaac cagttctgcg attagacaat gcaccggAACCTT cttatgatgt 1200
gagttttggg aattcttagct actacaatcc aactttgaat gattcagcca 1250
tgccagaaag tgaagaaaaat gcacgtgatg gcatttcatttggatgacata 1300
cctccacttc gtacttctgt atagaactaa cagaaaaag gcgttaaaca 1350
gcaagtgtca tctacatcct agcctttga caaattcatttca tttcaaaaagg 1400
ttacacaaaaa ttactgtcac gtggatttttgc tcaaggagaa tcataaaagc 1450
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tttcttacaa tttttggcca tcctgaggca tttactaagt agccttaatttgc 1550
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aactaaaaaga ttccaccattt acagccctgc ctcataacta aataataaaa 1650
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tgcctgaagc cctagtagacca taattcaaga ttgcattttc ttaaatgaaa 1750

attgaaaggg tgcttttaa agaaaatttg acttaaagct aaaaagagga 1800
 catagcccag agtttctgtt attggaaat tgaggcaata gaaatgacag 1850
 acctgtattc tagtacgtta taatttcta gatcagcaca cacatgatca 1900
 gcccactgag ttatgaagct gacaatgact gcattcaacg gggccatggc 1950
 aggaaagctg accctaccca ggaaagtaat agcttctta aaagtctca 2000
 aaggtttgg gaatttaac ttgtcttaat atatcttagg cttcaattat 2050
 ttgggtgcct taaaaactca atgagaatca tggt 2084

<210> 41
 <211> 334
 <212> PRT
 <213> Homo sapiens

<400> 41
 Met Leu Ala Leu Ala Lys Ile Leu Leu Ile Ser Thr Leu Phe Tyr
 1 5 10 15

Ser Leu Leu Ser Gly Ser His Gly Lys Glu Asn Gln Asp Ile Asn
 20 25 30

Thr Thr Gln Asn Ile Ala Glu Val Phe Lys Thr Met Glu Asn Lys
 35 40 45

Pro Ile Ser Leu Glu Ser Glu Ala Asn Leu Asn Ser Asp Lys Glu
 50 55 60

Asn Ile Thr Thr Ser Asn Leu Lys Ala Ser His Ser Pro Pro Leu
 65 70 75

Asn Leu Pro Asn Asn Ser His Gly Ile Thr Asp Phe Ser Ser Asn
 80 85 90

Ser Ser Ala Glu His Ser Leu Gly Ser Leu Lys Pro Thr Ser Thr
 95 100 105

Ile Ser Thr Ser Pro Pro Leu Ile His Ser Phe Val Ser Lys Val
 110 115 120

Pro Trp Asn Ala Pro Ile Ala Asp Glu Asp Leu Leu Pro Ile Ser
 125 130 135

Ala His Pro Asn Ala Thr Pro Ala Leu Ser Ser Glu Asn Phe Thr
 140 145 150

Trp Ser Leu Val Asn Asp Thr Val Lys Thr Pro Asp Asn Ser Ser
 155 160 165

Ile Thr Val Ser Ile Leu Ser Ser Glu Pro Thr Ser Pro Ser Val
 170 175 180

Thr Pro Leu Ile Val Glu Pro Ser Gly Trp Leu Thr Thr Asn Ser
 185 190 195

Asp Ser Phe Thr Gly Phe Thr Pro Tyr Gln Glu Lys Thr Thr Leu
 200 205 210
 Gln Pro Thr Leu Lys Phe Thr Asn Asn Ser Lys Leu Phe Pro Asn
 215 220 225
 Thr Ser Asp Pro Gln Lys Glu Asn Arg Asn Thr Gly Ile Val Phe
 230 235 240
 Gly Ala Ile Leu Gly Ala Ile Leu Gly Val Ser Leu Leu Thr Leu
 245 250 255
 Val Gly Tyr Leu Leu Cys Gly Lys Arg Lys Thr Asp Ser Phe Ser
 260 265 270
 His Arg Arg Leu Tyr Asp Asp Arg Asn Glu Pro Val Leu Arg Leu
 275 280 285
 Asp Asn Ala Pro Glu Pro Tyr Asp Val Ser Phe Gly Asn Ser Ser
 290 295 300
 Tyr Tyr Asn Pro Thr Leu Asn Asp Ser Ala Met Pro Glu Ser Glu
 305 310 315
 Glu Asn Ala Arg Asp Gly Ile Pro Met Asp Asp Ile Pro Pro Leu
 320 325 330
 Arg Thr Ser Val

<210> 42
 <211> 1594
 <212> DNA
 <213> Homo sapiens

<400> 42
 aacaggatct cctcttgcag tctgcagccc aggacgctga ttccagcagc 50
 gccttaccgc gcagccccaa gattcactat ggtgaaaatc gccttcaata 100
 ccccttaccgc cgtcaaaaag gaggaggcgc ggcaagacgt ggaggccctc 150
 ctgagccgca cggtcagaac tcaagatactg accggcaagg agctccgagt 200
 tgccacccag gaaaaagagg gtcctctgg gagatgtatg cttactctct 250
 taggcctttc attcatcttg gcaggactta ttgttggtgg agcctgcatt 300
 tacaagtact tcatgcccaa gagcaccatt taccgtggag agatgtgctt 350
 ttgttattctt gaggatcctg caaattccct tcgtggagga gaggcttaact 400
 tcctgcctgt gactgaggag gctgacattc gtgaggatga caacattgca 450
 atcattgtatg tgcctgtccc cagtttctct gatagtgacc ctgcagcaat 500
 tattcatgac tttgaaaaagg gaatgactgc ttacctggac ttgttgcctgg 550

ggaactgcta tctgatgccc ctcaataactt ctattgttat gcctccaaaa 600
aatctggtag agctcttgg caaactggcg agtggcagat atctgcctca 650
aacttatgtg gttcgagaag acctagttgc tgtggaggaa attcgtatg 700
ttagtaacct tggcatctt atttaccaac tttgcaataa cagaaagtcc 750
ttccgccttc gtcgcagaga cctcttgctg ggttcaaca aacgtgccat 800
tgataaatgc tggaagatta gacacttccc caacgaattt attgttgaga 850
ccaagatctg tcaagagtaa gaggcaacag atagagtgtc cttggtaata 900
agaagtcaga gatttacaat atgacttaa cattaaggaa tatgggatac 950
tcaagatatt tactcatgca tttactctat tgcttatgct taaaaaaaaag 1000
aaaaaaaaaa aaaactacta accactgcaa gctcttgtca aatttttagtt 1050
taattggcat tgcttgaaaa ttgaaactga aattacatga gtttcatttt 1100
ttctttgcat ttatagggtt tagatttctg aaagcagcat gaatatatca 1150
cctaacatcc tgacaataaa ttccatccgt tgttttttt gtttgggttt 1200
tttttctttt ccttaagta agctctttat tcacatctatg gtggagcaat 1250
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tatcagatct caacattgtt gttttctttt gtttttcatt ttgtacaact 1350
ttcttgaatt tagaaattac atctttgcag ttctgttagg tgctctgtaa 1400
ttaacctgac ttatatgtga acaattttca tgagacagtc attttaact 1450
aatgcagtga ttcttctca ctactatctg tatttgaa tgccaaaaat 1500
tgtgttaggtg ctgaatgctg taaggagttt aggttgtatg aattctacaa 1550
ccctataata aattttactc tataaaaaaa aaaaaaaaaa aaaa 1594

<210> 43
<211> 263
<212> PRT
<213> Homo sapiens

<400> 43
Met Val Lys Ile Ala Phe Asn Thr Pro Thr Ala Val Gln Lys Glu
1 5 10 15
Glu Ala Arg Gln Asp Val Glu Ala Leu Leu Ser Arg Thr Val Arg
20 25 30
Thr Gln Ile Leu Thr Gly Lys Glu Leu Arg Val Ala Thr Gln Glu
35 40 45
Lys Glu Gly Ser Ser Gly Arg Cys Met Leu Thr Leu Leu Gly Leu

50	55	60
Ser Phe Ile Leu Ala Gly Leu Ile Val Gly Gly Ala Cys Ile Tyr		
65	70	75
Lys Tyr Phe Met Pro Lys Ser Thr Ile Tyr Arg Gly Glu Met Cys		
80	85	90
Phe Phe Asp Ser Glu Asp Pro Ala Asn Ser Leu Arg Gly Gly Glu		
95	100	105
Pro Asn Phe Leu Pro Val Thr Glu Glu Ala Asp Ile Arg Glu Asp		
110	115	120
Asp Asn Ile Ala Ile Ile Asp Val Pro Val Pro Ser Phe Ser Asp		
125	130	135
Ser Asp Pro Ala Ala Ile Ile His Asp Phe Glu Lys Gly Met Thr		
140	145	150
Ala Tyr Leu Asp Leu Leu Leu Gly Asn Cys Tyr Leu Met Pro Leu		
155	160	165
Asn Thr Ser Ile Val Met Pro Pro Lys Asn Leu Val Glu Leu Phe		
170	175	180
Gly Lys Leu Ala Ser Gly Arg Tyr Leu Pro Gln Thr Tyr Val Val		
185	190	195
Arg Glu Asp Leu Val Ala Val Glu Glu Ile Arg Asp Val Ser Asn		
200	205	210
Leu Gly Ile Phe Ile Tyr Gln Leu Cys Asn Asn Arg Lys Ser Phe		
215	220	225
Arg Leu Arg Arg Arg Asp Leu Leu Leu Gly Phe Asn Lys Arg Ala		
230	235	240
Ile Asp Lys Cys Trp Lys Ile Arg His Phe Pro Asn Glu Phe Ile		
245	250	255
Val Glu Thr Lys Ile Cys Gln Glu		
260		

<210> 44
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 44
 gaaagacacg acacagcagc ttgc 24

<210> 45

<211> 20
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-20
<223> Synthetic construct.

<400> 45
gggaactgct atctgatgcc 20

<210> 46
<211> 26
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-26
<223> Synthetic construct.

<400> 46
caggatctcc tcttgagtc tgcagc 26

<210> 47
<211> 28
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-28
<223> Synthetic construct.

<400> 47
cttctcgaac cacataagtt tgaggcag 28

<210> 48
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-25
<223> Synthetic construct.

<400> 48
cacgattccc tccacaccaa ctggg 25

<210> 49
<211> 1969
<212> DNA
<213> Homo sapiens

<400> 49
ggaggaggga gggcgggcag ggcgcagccc aggcgcagccc cgggcaccag 50

cacggactct ctcttccagc ccaggtgccc cccactctcg ctccattcgg 100
cgggagcacc cagtcctgta cgccaaggaa ctggcctgg gggcaccatg 150
gttcggcgg cagccccag ctcctcatac cttctgtgc tgctgctggg 200
gtctgtgcct gctaccgacg cccgctctgt gcccctgaag gccacgttcc 250
tggaggatgt ggccggtagt ggggaggccg agggctcgta ggcctcctcc 300
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ggctccctgg cttttctgct gatgttcatac gtctgtgccc cggtcatcac 500
ccggcagaag cagaaggcct cggcctattta cccatcgta ttccccaaga 550
agaagtacgt ggaccagagt gaccgggccc gggggccccc ggccttcaagt 600
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cagaaatgct ggtccccgt gccccggagg aatcttacca agtgcacca 1200
tccttcaccc cagcagcccc aaagggtac atcctacagc acagctcccc 1250
tgacaaatgtc agggagggca cgtgtccctg tgacagccag gataaaacat 1300
ccccccaaatgt gctgggatta caggcgtgag ccaccgtgcc cggcccaaac 1350
tacttttaa aacagctaca gggtaaaatc ctgcagcacc cactctggaa 1400
aatactgctc ttaattttcc tgaaggtggc cccctgtttc tagttggtcc 1450
aggatttaggg atgtggggta tagggcattt aaatcccttc aagcgctctc 1500

caagcacccc cggcctgggg gtgagttct catcccgcta ctgctgctgg 1550
gatcaggttg aatgaatgga actcttcctg tctggcctcc aaagcagcct 1600
agaagctgag gggctgtgtt tgaggggacc tccaccctgg ggaagtccga 1650
ggggctgggg aagggttct gacgcccagc ctggagcagg gggccctgg 1700
ccacccctg ttgctcacac attgtctggc agcctgtgtc cacaatattc 1750
gtcagtcctc gacagggagc ctgggctccg tcctgctta gggaggctct 1800
ggcaggaggt cctctccccc atccctccat ctgggctcc cccaacctct 1850
gcacagctct ccaggtgctg agatataatg caccagcaca ataaaccttt 1900
attccggcct gaaaaaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa 1950
aaaaaaaaaaa aaaaaaaga 1969

<210> 50
<211> 283
<212> PRT
<213> Homo sapiens

<400> 50
Met Val Ser Ala Ala Ala Pro Ser Leu Leu Ile Leu Leu Leu Leu
1 5 10 15
Leu Leu Gly Ser Val Pro Ala Thr Asp Ala Arg Ser Val Pro Leu
20 25 30
Lys Ala Thr Phe Leu Glu Asp Val Ala Gly Ser Gly Glu Ala Glu
35 40 45
Gly Ser Ser Ala Ser Ser Pro Ser Leu Pro Pro Pro Trp Thr Pro
50 55 60
Ala Leu Ser Pro Thr Ser Met Gly Pro Gln Pro Thr Thr Leu Gly
65 70 75
Gly Pro Ser Pro Pro Thr Asn Phe Leu Asp Gly Ile Val Asp Phe
80 85 90
Phe Arg Gln Tyr Val Met Leu Ile Ala Val Val Gly Ser Leu Ala
95 100 105
Phe Leu Leu Met Phe Ile Val Cys Ala Ala Val Ile Thr Arg Gln
110 115 120
Lys Gln Lys Ala Ser Ala Tyr Tyr Pro Ser Ser Phe Pro Lys Lys
125 130 135
Lys Tyr Val Asp Gln Ser Asp Arg Ala Gly Gly Pro Arg Ala Phe
140 145 150
Ser Glu Val Pro Asp Arg Ala Pro Asp Ser Arg Pro Glu Glu Ala
155 160 165

Leu Asp Ser Ser Arg Gln Leu Gln Ala Asp Ile Leu Ala Ala Thr
170 175 180
Gln Asn Leu Lys Ser Pro Thr Arg Ala Ala Leu Gly Gly Gly Asp
185 190 195
Gly Ala Arg Met Val Glu Gly Arg Gly Ala Glu Glu Glu Glu Lys
200 205 210
Gly Ser Gln Glu Gly Asp Gln Glu Val Gln Gly His Gly Val Pro
215 220 225
Val Glu Thr Pro Glu Ala Gln Glu Glu Pro Cys Ser Gly Val Leu
230 235 240
Glu Gly Ala Val Val Ala Gly Glu Gly Gln Gly Glu Leu Glu Gly
245 250 255
Ser Leu Leu Leu Ala Gln Glu Ala Gln Gly Pro Val Gly Pro Pro
260 265 270
Glu Ser Pro Cys Ala Cys Ser Ser Val His Pro Ser Val
275 280

<210> 51
<211> 1734
<212> DNA
<213> Homo sapiens

<400> 51
gtggactctg agaagccag gcagttgagg acaggagaga gaaggctgca 50
gacccagagg gagggaggac agggagtcgg aaggaggagg acagaggagg 100
gcacagagac gcagagcaag ggcggcaagg aggagaccct ggtgggagga 150
agacactctg gagagagagg gggctggca gagatgaagt tccaggggcc 200
cctggcctgc ctcctgctgg ccctctgcct gggcagtggg gaggctggcc 250
ccctgcagag cggagaggaa agcactggga caaatattgg ggaggccctt 300
ggacatggcc tgggagacgc cctgagcgaa ggggtggaa aggccattgg 350
caaagaggcc ggagggcag ctggctctaa agtcagttag gcccattggcc 400
aagggaccag agaagcagtt ggcactggag tcaggcaggt tccaggctt 450
ggcgcagcag atgcttggg caacagggtc gggaaagcag cccatgctct 500
ggaaacact gggcacgaga ttggcagaca ggcagaagat gtcattcgac 550
acggagcaga tgctgtccgc ggctcctggc aggggtggcc tggccacagt 600
ggtgcttggg aaacttctgg aggccatggc atcttggct ctaaggtgg 650
ccttggaggg cagggccagg gcaatcctgg aggtctgggg actccgtggg 700

tccacggata ccccgaaac tcagcaggca gcttggaaat gaatcctcag 750
ggagctccct ggggtcaagg aggcaatggaa gggccaccaa actttggac 800
caacactcag ggagctgtgg cccagcctgg ctatggttca gtgagagcca 850
gcaaccagaa tgaagggtgc acgaatcccc caccatctgg ctcaggtgga 900
ggctccagca actctggggg aggcaagcggc tcacagtcgg gcagcagtgg 950
cagtggcagc aatggtgaca acaacaatgg cagcagcagt ggtggcagca 1000
gcagtggcag cagcaagtggc agcagcagtgc gcggcagcag tggcggcagc 1050
agtggtgca gcagtggcaa cagtggtggc agcagaggtg acagcggcag 1100
tgagtccctcc tgggatcca gcaccggctc ctccctccggc aaccacggtg 1150
ggagcggcgg agaaatggaa cataaaccgg ggtgtgaaaa gccagggaaat 1200
gaagcccgcg ggagcggggaa atctgggatt cagggcttca gaggacaggg 1250
agtttccagc aacatgaggg aaataagcaa agagggcaat cgcctccttg 1300
gaggctctgg agacaattat cggggcaag ggtcgagctg gggcagtgg 1350
ggaggtgacg ctgttggtgg agtcaatact gtgaactctg agacgtctcc 1400
tggatgttt aactttgaca ctttctggaa gaattttaaa tccaagctgg 1450
gtttcatcaa ctggatgcc ataaacaagg accagagaag ctctcgcatc 1500
ccgtgacctc cagacaagga gccaccagat tggatggag ccccccacact 1550
ccctccctaa aacaccaccc tctcatcaact aatctcagcc cttgccttg 1600
aaataaacct tagctgcccc aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1650
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1700
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1734

<210> 52

<211> 440

<212> PRT

<213> Homo sapiens

<400> 52

Met Lys Phe Gln Gly Pro Leu Ala Cys Leu Leu Leu Ala Leu Cys
1 5 10 15

Leu Gly Ser Gly Glu Ala Gly Pro Leu Gln Ser Gly Glu Glu Ser
20 25 30

Thr Gly Thr Asn Ile Gly Glu Ala Leu Gly His Gly Leu Gly Asp
35 40 45

Ala Leu Ser Glu Gly Val Gly Lys Ala Ile Gly Lys Glu Ala Gly

50	55	60
Gly Ala Ala Gly Ser Lys Val Ser Glu Ala	Leu Gly Gln Gly Thr	
65	70	75
Arg Glu Ala Val Gly Thr Gly Val Arg Gln	Val Pro Gly Phe Gly	
80	85	90
Ala Ala Asp Ala Leu Gly Asn Arg Val Gly	Glu Ala Ala His Ala	
95	100	105
Leu Gly Asn Thr Gly His Glu Ile Gly Arg	Gln Ala Glu Asp Val	
110	115	120
Ile Arg His Gly Ala Asp Ala Val Arg Gly	Ser Trp Gln Gly Val	
125	130	135
Pro Gly His Ser Gly Ala Trp Glu Thr Ser	Gly Gly His Gly Ile	
140	145	150
Phe Gly Ser Gln Gly Gly Leu Gly Gly Gln	Gly Gln Gly Asn Pro	
155	160	165
Gly Gly Leu Gly Thr Pro Trp Val His Gly	Tyr Pro Gly Asn Ser	
170	175	180
Ala Gly Ser Phe Gly Met Asn Pro Gln Gly	Ala Pro Trp Gly Gln	
185	190	195
Gly Gly Asn Gly Gly Pro Pro Asn Phe Gly	Thr Asn Thr Gln Gly	
200	205	210
Ala Val Ala Gln Pro Gly Tyr Gly Ser Val	Arg Ala Ser Asn Gln	
215	220	225
Asn Glu Gly Cys Thr Asn Pro Pro Pro Ser	Gly Ser Gly Gly Gly	
230	235	240
Ser Ser Asn Ser Gly Gly Ser Gly Ser Gln	Ser Gly Ser Ser Ser	
245	250	255
Gly Ser Gly Ser Asn Gly Asp Asn Asn Asn	Gly Ser Ser Ser Ser	
260	265	270
Gly Ser Ser Ser Gly Ser Ser Ser Gly Ser	Ser Ser Gly Gly Ser	
275	280	285
Ser Gly Gly Ser Ser Gly Ser Ser Gly Asn	Ser Ser Gly Gly Ser	
290	295	300
Arg Gly Asp Ser Gly Ser Glu Ser Ser Trp	Gly Ser Ser Thr Gly	
305	310	315
Ser Ser Ser Gly Asn His Gly Gly Ser Gly	Gly Gly Asn Gly His	
320	325	330
Lys Pro Gly Cys Glu Lys Pro Gly Asn Glu	Ala Arg Gly Ser Gly	
335	340	345

Glu Ser Gly Ile Gln Gly Phe Arg Gly Gln Gly Val Ser Ser Asn
350 355 360
Met Arg Glu Ile Ser Lys Glu Gly Asn Arg Leu Leu Gly Gly Ser
365 370 375
Gly Asp Asn Tyr Arg Gly Gln Gly Ser Ser Trp Gly Ser Gly Gly
380 385 390
Gly Asp Ala Val Gly Gly Val Asn Thr Val Asn Ser Glu Thr Ser
395 400 405
Pro Gly Met Phe Asn Phe Asp Thr Phe Trp Lys Asn Phe Lys Ser
410 415 420
Lys Leu Gly Phe Ile Asn Trp Asp Ala Ile Asn Lys Asp Gln Arg
425 430 435
Ser Ser Arg Ile Pro
440

<210> 53
<211> 3580
<212> DNA
<213> Homo sapiens

<400> 53
gaccgggtccc tccgggcctg gatgtgcgga ctctgctgca gcgagggctg 50
caggccccgcc gggcggtgct caccgtgccc tggctggtgg agtttctctc 100
ctttgctgac catgttgttc ctttgctgga atattaccgg gacatcttca 150
ctctcctgct gcgcctgcac cggagcttgg tgggtgcga ggagagttag 200
ggaaagatgt gtttcctgaa caagctgctg ctacttgctg tcctgggctg 250
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<212> PRT
<213> Homo sapiens

<400> 54

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<212> DNA
<213> Homo sapiens

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<212> PRT
<213> Homo sapiens

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<211> 1115

<212> PRT

<213> Homo sapiens

<400> 58

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					35				40				45	
Val	Gln	Lys	Pro	Gly	Gly	Thr	Val	Ile	Leu	Gly	Cys	Val	Val	Glu
				50					55				60	
Pro	Pro	Arg	Met	Asn	Val	Thr	Trp	Arg	Leu	Asn	Gly	Lys	Glu	Leu
					65				70				75	
Asn	Gly	Ser	Asp	Asp	Ala	Leu	Gly	Val	Leu	Ile	Thr	His	Gly	Thr
					80				85				90	
Leu	Val	Ile	Thr	Ala	Leu	Asn	Asn	His	Thr	Val	Gly	Arg	Tyr	Gln
					95				100				105	
Cys	Val	Ala	Arg	Met	Pro	Ala	Gly	Ala	Val	Ala	Ser	Val	Pro	Ala
					110				115				120	
Thr	Val	Thr	Leu	Ala	Asn	Leu	Gln	Asp	Phe	Lys	Leu	Asp	Val	Gln
					125				130				135	
His	Val	Ile	Glu	Val	Asp	Glu	Gly	Asn	Thr	Ala	Val	Ile	Ala	Cys
					140				145				150	
His	Leu	Pro	Glu	Ser	His	Pro	Lys	Ala	Gln	Val	Arg	Tyr	Ser	Val
					155				160				165	
Lys	Gln	Glu	Trp	Leu	Glu	Ala	Ser	Arg	Gly	Asn	Tyr	Leu	Ile	Met
					170				175				180	
Pro	Ser	Gly	Asn	Leu	Gln	Ile	Val	Asn	Ala	Ser	Gln	Glu	Asp	Glu
					185				190				195	
Gly	Met	Tyr	Lys	Cys	Ala	Ala	Tyr	Asn	Pro	Val	Thr	Gln	Glu	Val
					200				205				210	
Lys	Thr	Ser	Gly	Ser	Ser	Asp	Arg	Leu	Arg	Val	Arg	Arg	Ser	Thr
					215				220				225	
Ala	Glu	Ala	Ala	Arg	Ile	Ile	Tyr	Pro	Pro	Glu	Ala	Gln	Thr	Ile
					230				235				240	
Ile	Val	Thr	Lys	Gly	Gln	Ser	Leu	Ile	Leu	Glu	Cys	Val	Ala	Ser
					245				250				255	
Gly	Ile	Pro	Pro	Pro	Arg	Val	Thr	Trp	Ala	Lys	Asp	Gly	Ser	Ser
					260				265				270	

Val Thr Gly Tyr Asn Lys Thr Arg Phe Leu Leu Ser Asn Leu Leu
 275 280 285
 Ile Asp Thr Thr Ser Glu Glu Asp Ser Gly Thr Tyr Arg Cys Met
 290 295 300
 Ala Asp Asn Gly Val Gly Gln Pro Gly Ala Ala Val Ile Leu Tyr
 305 310 315
 Asn Val Gln Val Phe Glu Pro Pro Glu Val Thr Met Glu Leu Ser
 320 325 330
 Gln Leu Val Ile Pro Trp Gly Gln Ser Ala Lys Leu Thr Cys Glu
 335 340 345
 Val Arg Gly Asn Pro Pro Pro Ser Val Leu Trp Leu Arg Asn Ala
 350 355 360
 Val Pro Leu Ile Ser Ser Gln Arg Leu Arg Leu Ser Arg Arg Ala
 365 370 375
 Leu Arg Val Leu Ser Met Gly Pro Glu Asp Glu Gly Val Tyr Gln
 380 385 390
 Cys Met Ala Glu Asn Glu Val Gly Ser Ala His Ala Val Val Gln
 395 400 405
 Leu Arg Thr Ser Arg Pro Ser Ile Thr Pro Arg Leu Trp Gln Asp
 410 415 420
 Ala Glu Leu Ala Thr Gly Thr Pro Pro Val Ser Pro Ser Lys Leu
 425 430 435
 Gly Asn Pro Glu Gln Met Leu Arg Gly Gln Pro Ala Leu Pro Arg
 440 445 450
 Pro Pro Thr Ser Val Gly Pro Ala Ser Pro Lys Cys Pro Gly Glu
 455 460 465
 Lys Gly Gln Gly Ala Pro Ala Glu Ala Pro Ile Ile Leu Ser Ser
 470 475 480
 Pro Arg Thr Ser Lys Thr Asp Ser Tyr Glu Leu Val Trp Arg Pro
 485 490 495
 Arg His Glu Gly Ser Gly Arg Ala Pro Ile Leu Tyr Tyr Val Val
 500 505 510
 Lys His Arg Lys Gln Val Thr Asn Ser Ser Asp Asp Trp Thr Ile
 515 520 525
 Ser Gly Ile Pro Ala Asn Gln His Arg Leu Thr Leu Thr Arg Leu
 530 535 540
 Asp Pro Gly Ser Leu Tyr Glu Val Glu Met Ala Ala Tyr Asn Cys
 545 550 555
 Ala Gly Glu Gly Gln Thr Ala Met Val Thr Phe Arg Thr Gly Arg

560	565	570
Arg Pro Lys Pro Glu Ile Met Ala Ser	Lys Glu Gln Gln Ile Gln	
575	580	585
Arg Asp Asp Pro Gly Ala Ser Pro Gln	Ser Ser Ser Gln Pro Asp	
590	595	600
His Gly Arg Leu Ser Pro Pro Glu Ala	Pro Asp Arg Pro Thr Ile	
605	610	615
Ser Thr Ala Ser Glu Thr Ser Val Tyr	Val Thr Trp Ile Pro Arg	
620	625	630
Gly Asn Gly Gly Phe Pro Ile Gln Ser	Phe Arg Val Glu Tyr Lys	
635	640	645
Lys Leu Lys Lys Val Gly Asp Trp Ile	Leu Ala Thr Ser Ala Ile	
650	655	660
Pro Pro Ser Arg Leu Ser Val Glu Ile	Thr Gly Leu Glu Lys Gly	
665	670	675
Thr Ser Tyr Lys Phe Arg Val Arg Ala	Leu Asn Met Leu Gly Glu	
680	685	690
Ser Glu Pro Ser Ala Pro Ser Arg Pro	Tyr Val Val Ser Gly Tyr	
695	700	705
Ser Gly Arg Val Tyr Glu Arg Pro Val	Ala Gly Pro Tyr Ile Thr	
710	715	720
Phe Thr Asp Ala Val Asn Glu Thr Thr	Ile Met Leu Lys Trp Met	
725	730	735
Tyr Ile Pro Ala Ser Asn Asn Asn Thr	Pro Ile His Gly Phe Tyr	
740	745	750
Ile Tyr Tyr Arg Pro Thr Asp Ser Asp	Asn Asp Ser Asp Tyr Lys	
755	760	765
Lys Asp Met Val Glu Gly Asp Lys Tyr	Trp His Ser Ile Ser His	
770	775	780
Leu Gln Pro Glu Thr Ser Tyr Asp Ile	Lys Met Gln Cys Phe Asn	
785	790	795
Glu Gly Gly Glu Ser Glu Phe Ser Asn	Val Met Ile Cys Glu Thr	
800	805	810
Lys Ala Arg Lys Ser Ser Gly Gln Pro	Gly Arg Leu Pro Pro Pro	
815	820	825
Thr Leu Ala Pro Pro Gln Pro Pro Leu	Pro Glu Thr Ile Glu Arg	
830	835	840
Pro Val Gly Thr Gly Ala Met Val Ala	Arg Ser Ser Asp Leu Pro	
845	850	855

Tyr Leu Ile Val Gly Val Val Leu Gly Ser Ile Val Leu Ile Ile
 860 865 870
 Val Thr Phe Ile Pro Phe Cys Leu Trp Arg Ala Trp Ser Lys Gln
 875 880 885
 Lys His Thr Thr Asp Leu Gly Phe Pro Arg Ser Ala Leu Pro Pro
 890 895 900
 Ser Cys Pro Tyr Thr Met Val Pro Leu Gly Gly Leu Pro Gly His
 905 910 915
 Gln Ala Ser Gly Gln Pro Tyr Leu Ser Gly Ile Ser Gly Arg Ala
 920 925 930
 Cys Ala Asn Gly Ile His Met Asn Arg Gly Cys Pro Ser Ala Ala
 935 940 945
 Val Gly Tyr Pro Gly Met Lys Pro Gln Gln His Cys Pro Gly Glu
 950 955 960
 Leu Gln Gln Gln Ser Asp Thr Ser Ser Leu Leu Arg Gln Thr His
 965 970 975
 Leu Gly Asn Gly Tyr Asp Pro Gln Ser His Gln Ile Thr Arg Gly
 980 985 990
 Pro Lys Ser Ser Pro Asp Glu Gly Ser Phe Leu Tyr Thr Leu Pro
 995 1000 1005
 Asp Asp Ser Thr His Gln Leu Leu Gln Pro His His Asp Cys Cys
 1010 1015 1020
 Gln Arg Gln Glu Gln Pro Ala Ala Val Gly Gln Ser Gly Val Arg
 1025 1030 1035
 Arg Ala Pro Asp Ser Pro Val Leu Glu Ala Val Trp Asp Pro Pro
 1040 1045 1050
 Phe His Ser Gly Pro Pro Cys Cys Leu Gly Leu Val Pro Val Glu
 1055 1060 1065
 Glu Val Asp Ser Pro Asp Ser Cys Gln Val Ser Gly Gly Asp Trp
 1070 1075 1080
 Cys Pro Gln His Pro Val Gly Ala Tyr Val Gly Gln Glu Pro Gly
 1085 1090 1095
 Met Gln Leu Ser Pro Gly Pro Leu Val Arg Val Ser Phe Glu Thr
 1100 1105 1110
 Pro Pro Leu Thr Ile
 1115

<210> 59
 <211> 25
 <212> DNA
 <213> Artificial

<220>
<221> Artificial sequence
<222> 1-25
<223> Synthetic construct.

<400> 59
gggaaacaca gcagtcattg cctgc 25

<210> 60
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-24
<223> Synthetic construct.

<400> 60
gcacacgtag cctgtcgctg gagc 24

<210> 61
<211> 42
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-42
<223> Synthetic construct.

<400> 61
caccccaaag cccaggtccg gtacagcgtc aaacaagagt gg 42

<210> 62
<211> 1661
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 678
<223> unknown base

<400> 62
cgggaggctg ggtcgcatg atccggaccc cattgtcgcc ctctgccc 50
cgccctgctcc tcccaggctc ccgcggccga ccccccgcga acatgcagcc 100
cacggggccgc gagggttccc ggcgcgtca g cggcggtat ctgcggcg 150
tgctgctcct gctactgctg ctgctgctgc ggcagccgt aaccgcgcg 200
gagaccacgc cggcgcccc cagagccctc tccacgctgg gctccccag 250
cctcttcacc acgcccgggtg tccccagcgc cctcaactacc ccaggcctca 300
ctacgccagg caccccaaa accctggacc ttcgggtcg cgccgaggcc 350

ctgatgcgga gtttccact cgtggacggc cacaatgacc tgccccaggt 400
cctgagacag cgttacaaga atgtgcttca ggatgttaac ctgcgaaatt 450
tcagccatgg tcagaccagc ctggacaggc ttagagacgg cctcgtgggt 500
gcccgaggttct ggtcagcctc cgtctcatgc cagtcggcagg accagactgc 550
cgtgcgcctc gcccctggagc agattgaccc tattcaccgc atgtgtgcct 600
ccctactctga actcgagctt gtgacctcag ctgaaggctc gaacagctct 650
caaaaagctgg cctgcctcat tggcgtgnag ggtggtaact cactggacag 700
cagcctctct gtgctgcgca gtttctatgt gctgggggtg cgctacctga 750
cacttacctt cacctgcagt acaccatggg cagagagttc caccaagttc 800
agacaccaca tgtacaccaa cgtcagcggga ttgacaagct ttggtgagaa 850
agtagtagag gagttgaacc gcctgggcat gatgatagat ttgtcctatg 900
catcggacac cttgataaga agggcctgg aagtgtctca ggctcctgtg 950
atcttctccc actcagctgc cagagctgtg tgtgacaatt tggtaatgt 1000
tcccgatgat atcctgcagc ttctgaagaa cgggtggcatc gtgatggta 1050
cactgtccat gggggtgctg cagtgcacc tgcttgctaa cgtgtccact 1100
gtggcagatc actttgacca catcaggcga gtcattggat ctgagttcat 1150
cgggattgggt gaaattatg acgggactgg ccgggtccct caggggctgg 1200
aggatgtgtc cacataacca gtcctgatag aggagttgct gagtcgtasc 1250
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cttcagacaa gtggaaaagg tgagagagga gagcaggcgc cagagcccc 1350
tggaggctga gtttccatat gggcaactga gcacatcctg ccactcccac 1400
ctcgtgcctc agaatggaca ccaggctact catctggagg tgaccaagca 1450
gccaaccaat cgggtccct ggaggtcctc aaatgcctcc ccataccttg 1500
ttccaggcct tgtggctgct gccaccatcc caaccttcac ccagtggctc 1550
tgctgacaca gtcggcccc gcagaggtca ctgtggcaaa gcctcacaaa 1600
gccccctctc ctatgttca cacaagcata tgctgagaat aaacatgtta 1650
cacatggaaa a 1661

<210> 63
<211> 487
<212> PRT
<213> Homo sapiens

<220>
<221> unsure
<222> 196, 386
<223> unknown amino acid

<400> 63

Met	Gln	Pro	Thr	Gly	Arg	Glu	Gly	Ser	Arg	Ala	Leu	Ser	Arg	Arg
1				5				10					15	
Tyr	Leu	Arg	Arg	Leu	Arg									
				20				25					30	
Gln	Pro	Val	Thr	Arg	Ala	Glu	Thr	Thr	Pro	Gly	Ala	Pro	Arg	Ala
				35				40					45	
Leu	Ser	Thr	Leu	Gly	Ser	Pro	Ser	Leu	Phe	Thr	Thr	Pro	Gly	Val
				50				55					60	
Pro	Ser	Ala	Leu	Thr	Thr	Pro	Gly	Leu	Thr	Thr	Pro	Gly	Thr	Pro
				65				70					75	
Lys	Thr	Leu	Asp	Leu	Arg	Gly	Arg	Ala	Gln	Ala	Leu	Met	Arg	Ser
				80				85					90	
Phe	Pro	Leu	Val	Asp	Gly	His	Asn	Asp	Leu	Pro	Gln	Val	Leu	Arg
				95				100					105	
Gln	Arg	Tyr	Lys	Asn	Val	Leu	Gln	Asp	Val	Asn	Leu	Arg	Asn	Phe
				110				115					120	
Ser	His	Gly	Gln	Thr	Ser	Leu	Asp	Arg	Leu	Arg	Asp	Gly	Leu	Val
				125				130					135	
Gly	Ala	Gln	Phe	Trp	Ser	Ala	Ser	Val	Ser	Cys	Gln	Ser	Gln	Asp
				140				145					150	
Gln	Thr	Ala	Val	Arg	Leu	Ala	Leu	Glu	Gln	Ile	Asp	Leu	Ile	His
				155				160					165	
Arg	Met	Cys	Ala	Ser	Tyr	Ser	Glu	Leu	Glu	Leu	Val	Thr	Ser	Ala
				170				175					180	
Glu	Gly	Leu	Asn	Ser	Ser	Gln	Lys	Leu	Ala	Cys	Leu	Ile	Gly	Val
				185				190					195	
Xaa	Gly	Gly	His	Ser	Leu	Asp	Ser	Ser	Leu	Ser	Val	Leu	Arg	Ser
				200				205					210	
Phe	Tyr	Val	Leu	Gly	Val	Arg	Tyr	Leu	Thr	Leu	Thr	Phe	Thr	Cys
				215				220					225	
Ser	Thr	Pro	Trp	Ala	Glu	Ser	Ser	Thr	Lys	Phe	Arg	His	His	Met
				230				235					240	
Tyr	Thr	Asn	Val	Ser	Gly	Leu	Thr	Ser	Phe	Gly	Glu	Lys	Val	Val
				245				250					255	
Glu	Glu	Leu	Asn	Arg	Leu	Gly	Met	Met	Ile	Asp	Leu	Ser	Tyr	Ala

260	265	270
Ser Asp Thr Leu Ile Arg Arg Val Leu Glu Val Ser Gln Ala Pro		
275	280	285
Val Ile Phe Ser His Ser Ala Ala Arg Ala Val Cys Asp Asn Leu		
290	295	300
Leu Asn Val Pro Asp Asp Ile Leu Gln Leu Leu Lys Asn Gly Gly		
305	310	315
Ile Val Met Val Thr Leu Ser Met Gly Val Leu Gln Cys Asn Leu		
320	325	330
Leu Ala Asn Val Ser Thr Val Ala Asp His Phe Asp His Ile Arg		
335	340	345
Ala Val Ile Gly Ser Glu Phe Ile Gly Ile Gly Gly Asn Tyr Asp		
350	355	360
Gly Thr Gly Arg Phe Pro Gln Gly Leu Glu Asp Val Ser Thr Tyr		
365	370	375
Pro Val Leu Ile Glu Glu Leu Leu Ser Arg Xaa Trp Ser Glu Glu		
380	385	390
Glu Leu Gln Gly Val Leu Arg Gly Asn Leu Leu Arg Val Phe Arg		
395	400	405
Gln Val Glu Lys Val Arg Glu Glu Ser Arg Ala Gln Ser Pro Val		
410	415	420
Glu Ala Glu Phe Pro Tyr Gly Gln Leu Ser Thr Ser Cys His Ser		
425	430	435
His Leu Val Pro Gln Asn Gly His Gln Ala Thr His Leu Glu Val		
440	445	450
Thr Lys Gln Pro Thr Asn Arg Val Pro Trp Arg Ser Ser Asn Ala		
455	460	465
Ser Pro Tyr Leu Val Pro Gly Leu Val Ala Ala Ala Thr Ile Pro		
470	475	480
Thr Phe Thr Gln Trp Leu Cys		
485		

<210> 64
 <211> 25
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial sequence
 <222> 1-25
 <223> Synthetic construct.

 <400> 64

ccttcacctg cagtacacca tgggc 25
 <210> 65
 <211> 25
 <212> DNA
 <213> Artificial
 <220>
 <221> Artificial sequence
 <222> 1-25
 <223> Synthetic construct.
 <400> 65
 gtcacacaca gctctggcag ctgag 25
 <210> 66
 <211> 47
 <212> DNA
 <213> Artificial
 <220>
 <221> Artificial sequence
 <222> 1-47
 <223> Synthetic construct.
 <400> 66
 ccaagttcag acaccacatg tacaccaacg tcagcggatt gacaaggc 47
 <210> 67
 <211> 1564
 <212> DNA
 <213> Homo sapiens
 <400> 67
 tgctaggctc tgtcccacaa tgcacccgag agcaggagct gaaaggcctct 50
 aacacccaca gatccctcta tgactgcaat gtgaggtgtc cggctttgct 100
 ggcccagcaa gcctgataag catgaagctc ttatcttgg tggctgtgtt 150
 cgggtgtttg ctggtgcccc cagctgaagc caacaagagt tctgaagata 200
 tccggtgcaa atgcacatgt ccaccttata gaaacatcag tggcacatt 250
 tacaaccaga atgtatccca gaaggactgc aactgcctgc acgtggtgaa 300
 gccccatgcca gtgcctggcc atgacgtgga ggcctactgc ctgctgtgcg 350
 agtgcaggta cgaggagcgc agcaccacca ccatcaaggt catcattgtc 400
 atctacatgt ccgtgggtgg tgcctgttg ctctacatgg ctttcctgat 450
 gctgggtggac cctctgatcc gaaagccgga tgcatacact gagcaactgc 500
 acaatgagga ggagaatgag gatgctcgct ctatggcagc agctgctgca 550
 tccctcgggg gaccccgagc aaacacagtc ctggagcgtg tggaaagggtgc 600

ccagcagcgg tggaaagctgc aggtgcagga gcagcggaaag acagtcttcg 650
atccggcacaa gatgctcagc tagatgggct ggtgtggttt ggtcaaggcc 700
ccaaacaccat ggctgccagc ttccaggctg gacaaagcag ggggctactt 750
ctcccttccc tcgggttccag tcttccctt aaaagcctgt ggcattttc 800
ctccttctcc ctaactttag aaatgttcta cttggctatt ttgatttaggg 850
aagagggatg tggtctctga tctctgttgt cttcttgggt ctttggggtt 900
gaagggaggg ggaaggcagg ccagaaggga atggagacat tcgaggcggc 950
ctcaggagtg gatgcgatct gtctctcctg gctccactct tgccgccttc 1000
cagctctgag tcttggaaat gttgttaccc ttggaagata aagctgggtc 1050
ttcaggaact cagtgtctgg gagggaaagca tggcccagca ttcagcatgt 1100
gttcctttct gcagtggttc ttatcaccac ctccctccca gccccggcgc 1150
ctcagccccca gccccagctc cagccctgag gacagctctg atgggagagc 1200
tgggccccct gagcccactg ggtcttcagg gtgcacttgg a gctgggttt 1250
cgctgtcccc t tgtcacttc tcgcacttgg gcatggagtg cccatgcata 1300
ctctgctgcc ggtccctca cctgcacttg aggggtctgg gcagtcctc 1350
ctctccccag t tgtccacagt cactgagcca gacggtcgg t ggaacatga 1400
gactcgaggc t tagcgttgg a tctgaacacc acagccccctg tacttgggtt 1450
gcctcttgta cctgaacttc gttgtaccag tgcattggaga gaaaattttg 1500
tctcttgta t tagagttgt gttgaaatca aggaagccat cattaaattt 1550
ttttatatttct ctca 1564

<210> 68
<211> 183
<212> PRT
<213> *Homo sapiens*

<400> 68

Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val
1 5 10 15

Pro Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys
20 25 30

Cys Ile Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn
 35 40 45

Gln Asn Val Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu
50 55 60

Pro Met Pro Val Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu
 65 70 75
 Cys Glu Cys Arg Tyr Glu Glu Arg Ser Thr Thr Thr Ile Lys Val
 80 85 90
 Ile Ile Val Ile Tyr Leu Ser Val Val Gly Ala Leu Leu Leu Tyr
 95 100 105
 Met Ala Phe Leu Met Leu Val Asp Pro Leu Ile Arg Lys Pro Asp
 110 115 120
 Ala Tyr Thr Glu Gln Leu His Asn Glu Glu Glu Asn Glu Asp Ala
 125 130 135
 Arg Ser Met Ala Ala Ala Ala Ser Leu Gly Gly Pro Arg Ala
 140 145 150
 Asn Thr Val Leu Glu Arg Val Glu Gly Ala Gln Gln Arg Trp Lys
 155 160 165
 Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe Asp Arg His Lys
 170 175 180
 Met Leu Ser

<210> 69
 <211> 3170
 <212> DNA
 <213> Homo sapiens

<400> 69
 agcgggtctc gcttgggttc cgctaatttc tgcctgagg cgtgagactg 50
 agttcatagg gtcctgggtc cccgaaccag gaagggttga gggAACACAA 100
 tctgcaagcc cccgcaccc aagtggggg ccccggttg gggcctccc 150
 tccctttgca ttcccACCC tccgggttt gcgtcttcct ggggACCCCC 200
 tcGCCGGGAG atggccgcgt tgcgtggag caaggattcg tcctgctgcc 250
 tgctcctact ggccgcgtg ctgtatggtgg agagtcaca gatcggcagt 300
 tcgcgggcca aactcaactc catcaagtcc tctctggcg gggagacgcc 350
 tggtcaggcc gccaatcgat ctgcgggcat gtaccaagga ctggcattcg 400
 gccgcgtaa gaaggcAAA aacctggggc aggcctaccc ttgttagcgt 450
 gataaggagt gtgaagttgg gaggtattgc cacagtcccc accaaggatc 500
 atcggcctgc atgggtgtgc ggagaaaaaa gaagcgctgc caccgagatg 550
 gcatgtgctg ccccagtacc cgctgcaata atggcatctg tatcccagtt 600
 actgaaagca tcttaACCC tcacatcccg gctctggatg gtactcggca 650

cagagatcga aaccacggtc attactcaa ccatgacttg ggatggcaga 700
atcttaggaag accacacact aagatgtcac atataaaagg gcatgaagga 750
gaccctgcc tacgatcatc agactgcatt gaagggttt gctgtgctcg 800
tcatttctgg accaaaatct gcaaaccagt gctccatca gggaaagtct 850
gtaccaaaca acgcaagaag gttctcatg ggctggaaat tttccagcgt 900
tgcgactgtg cgaagggcct gtcttgcaaa gtatggaaag atgccaccta 950
ctcctccaaa gccagactcc atgtgtgtca gaaaatttga tcaccattga 1000
ggaacatcat caattgcaga ctgtgaagtt gtgtattta tgcattata 1050
catggtgaa aataaggttc agatgcagaa gaatggctaa aataagaaac 1100
gtgataagaa tatagatgtat cacaaggagg gagaagaaa acatgaactg 1150
aatagattag aatgggtgac aaatgcagtg cagccagtgt ttccattatg 1200
caacttgtct atgtaaataa tgtacacatt tgtggaaat gctattatta 1250
agagaacaag cacacagtgg aaattactga tgagtagcat gtgactttcc 1300
aagagtttag gttgtgctgg aggagaggtt tccttcagat tgctgattgc 1350
ttatacaaataa aacctacatg ccagatttct attcaacgtt agagtttaac 1400
aaaatactcc tagaataact ttttatacaa taggttctaa aaataaaatt 1450
gctaaacaag aaatgaaaac atggagcatt gttatattac aacagaaaat 1500
taccttttga tttgtAACAC tacttctgt gttcaatcaa gagttttgtt 1550
agataagaaa aaaatcagtc aatatttcca aataattgca aaataatggc 1600
cagttgtta ggaaggcctt taggaagaca aataaataac aaacaaacag 1650
ccacaaatac tttttttca aaatttttagt ttacctgtt attaataaga 1700
actgatacaa gacaaaaaca gttccttcag attctacgga atgacagtat 1750
atctctcttt atcctatgtg attcctgctc tgaatgcatt atattttcca 1800
aactataccca ataaattgtg actagtaaaa tacttacaca gagcagaatt 1850
ttcacagatg gcaaaaaat ttaaagatgt ccaatatacg tggaaaaga 1900
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gatagaatta gattggtaaa tacatgtatt catacatact ctgtggtaat 2000
agagacttaa gctggatctg tactgcactg gagtaagcaa gaaaattggg 2050
aaaacttttt cgtttgttca gttttggca acacatagat catatgtctg 2100

aggcacaagt tggctgttca tctttgaaac cagggatgc acagtctaaa 2150
tgaatatctg catgggattt gctatcataa tatttactat gcagatgaat 2200
tcagtgttag gtcctgtgtc cgtactatcc tcaaattatt tattttatag 2250
tgctgagatc ctcaaataat ctcatttca ggaggttca caaaatgtac 2300
tcctgaagta gacagagtag tgaggttca ttgcctctta taagcttctg 2350
actagccaat ggcatcatcc aattttcttc ccaaacctct gcagcatctg 2400
ctttattgccc aaagggttag ttccggttt ctgcagccat tgccgttaaa 2450
aaatataagt aggataactt gtaaaacctg catattgcta atctatagac 2500
accacagttt ctaaattctt tgaaaccact ttactacttt ttttaaactt 2550
aactcagttc taaatacttt gtctggagca caaaacaata aaaggttac 2600
ttatagtcgt gactttaaac tttttagac cacaattcac ttttagttt 2650
tctttactt aaatcccatc tgcagtctca aatttaagtt ctccagtag 2700
agattgagtt tgagcctgta tatctattaa aaatttcaac ttcccacata 2750
tatttactaa gatgattaag acttacattt tctgcacagg tctgcaaaaa 2800
caaaaattat aaactagtcc atccaagaac caaagttgt ataaacaggt 2850
tgctataagc ttgtgaaatg aaaatgaaac atttcaatca aacatttcct 2900
atataacaat tattatattt acaatttggt ttctgcaata ttttcttat 2950
gtccaccctt taaaaaatta ttatttgaag taatttattt acaggaaatg 3000
ttaatgagat gtattttctt atagagatat ttcttacaga aagctttgta 3050
gcagaatata tttgcagcta ttgactttgt aatttagaa aatgtataa 3100
taagataaaaa tctattaaat ttttctcctc taaaaactga aaaaaaaaaa 3150
aaaaaaaaaaaa aaaaaaaaaa 3170

<210> 70
<211> 259
<212> PRT
<213> Homo sapiens

<400> 70
Met Ala Ala Leu Met Arg Ser Lys Asp Ser Ser Cys Cys Leu Leu
1 5 10 15
Leu Leu Ala Ala Val Leu Met Val Glu Ser Ser Gln Ile Gly Ser
20 25 30
Ser Arg Ala Lys Leu Asn Ser Ile Lys Ser Ser Leu Gly Gly Glu
35 40 45

Thr Pro Gly Gln Ala Ala Asn Arg Ser Ala Gly Met Tyr Gln Gly
 50 55 60
 Leu Ala Phe Gly Gly Ser Lys Lys Gly Lys Asn Leu Gly Gln Ala
 65 70 75
 Tyr Pro Cys Ser Ser Asp Lys Glu Cys Glu Val Gly Arg Tyr Cys
 80 85 90
 His Ser Pro His Gln Gly Ser Ser Ala Cys Met Val Cys Arg Arg
 95 100 105
 Lys Lys Lys Arg Cys His Arg Asp Gly Met Cys Cys Pro Ser Thr
 110 115 120
 Arg Cys Asn Asn Gly Ile Cys Ile Pro Val Thr Glu Ser Ile Leu
 125 130 135
 Thr Pro His Ile Pro Ala Leu Asp Gly Thr Arg His Arg Asp Arg
 140 145 150
 Asn His Gly His Tyr Ser Asn His Asp Leu Gly Trp Gln Asn Leu
 155 160 165
 Gly Arg Pro His Thr Lys Met Ser His Ile Lys Gly His Glu Gly
 170 175 180
 Asp Pro Cys Leu Arg Ser Ser Asp Cys Ile Glu Gly Phe Cys Cys
 185 190 195
 Ala Arg His Phe Trp Thr Lys Ile Cys Lys Pro Val Leu His Gln
 200 205 210
 Gly Glu Val Cys Thr Lys Gln Arg Lys Lys Gly Ser His Gly Leu
 215 220 225
 Glu Ile Phe Gln Arg Cys Asp Cys Ala Lys Gly Leu Ser Cys Lys
 230 235 240
 Val Trp Lys Asp Ala Thr Tyr Ser Ser Lys Ala Arg Leu His Val
 245 250 255
 Cys Gln Lys Ile

<210> 71
 <211> 1809
 <212> DNA
 <213> Homo sapiens

<400> 71
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 acatcacgtt tttaaaaatt gatttcttca aattcatggc aaatatttcc 150
 ctcccccttta acttcttatg tcagaatgag gaaggatagc tgcatttatt 200

tagtcagttt tcattgcata gtaatatttt catgtatcat tttctaagtt 250
atattttagt aattcatatg ttttagatta taggtttaa catacttg 300
aaaatactg atgtgtttta aagccttggg cagaaattct gtattgtga 350
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tttggagagc ttgcaccacc aaaaatggca aacatcacca gctcccagat 450
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gtacacagca gaatagtaca agtcacccta caactactac ttcttggac 550
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tgtctgtcca ccagccacag cccaaacaca tcaaacttgc taagcggcgg 850
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cttggggggg ccaaggcagg cagattgccca aagctcagga gtttgagacc 1650

accctggca acatggtaa actctgtctc tactaaaata cgaaaaacta 1700
 gccgggtgtg gtggcggcgc gtgcctgtaa tcccagctac ttgggaggct 1750
 gaggcacaag aatcgcttga gccagcttgg gctacaaagt gagactccgt 1800
 ctgaaaaga 1809

<210> 72
 <211> 363
 <212> PRT
 <213> Homo sapiens

<400> 72
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Cys Ser Phe Ile Pro Leu Leu Lys Ser Ser Val Leu Gly Ser Gly
 20 25 30

Phe Gly Glu Leu Ala Pro Pro Lys Met Ala Asn Ile Thr Ser Ser
 35 40 45

Gln Ile Leu Asp Gln Leu Lys Ala Pro Ser Leu Gly Gln Phe Thr
 50 55 60

Thr Thr Pro Ser Thr Gln Gln Asn Ser Thr Ser His Pro Thr Thr
 65 70 75

Thr Thr Ser Trp Asp Leu Lys Pro Pro Thr Ser Gln Ser Ser Val
 80 85 90

Leu Ser His Leu Asp Phe Lys Ser Gln Pro Glu Pro Ser Pro Val
 95 100 105

Leu Ser Gln Leu Ser Gln Arg Gln Gln His Gln Ser Gln Ala Val
 110 115 120

Thr Val Pro Pro Pro Gly Leu Glu Ser Phe Pro Ser Gln Ala Lys
 125 130 135

Leu Arg Glu Ser Thr Pro Gly Asp Ser Pro Ser Thr Val Asn Lys
 140 145 150

Leu Leu Gln Leu Pro Ser Thr Thr Ile Glu Asn Ile Ser Val Ser
 155 160 165

Val His Gln Pro Gln Pro Lys His Ile Lys Leu Ala Lys Arg Arg
 170 175 180

Ile Pro Pro Ala Ser Lys Ile Pro Ala Ser Ala Val Glu Met Pro
 185 190 195

Gly Ser Ala Asp Val Thr Gly Leu Asn Val Gln Phe Gly Ala Leu
 200 205 210

Glu Phe Gly Ser Glu Pro Ser Leu Ser Glu Phe Gly Ser Ala Pro
 215 220 225

Ser	Ser	Glu	Asn	Ser	Asn	Gln	Ile	Pro	Ile	Ser	Leu	Tyr	Ser	Lys	
230									235					240	
Ser	Leu	Ser	Glu	Pro	Leu	Asn	Thr	Ser	Leu	Ser	Met	Thr	Ser	Ala	
245									250					255	
Val	Gln	Asn	Ser	Thr	Tyr	Thr	Thr	Ser	Val	Ile	Thr	Ser	Cys	Ser	
	260								265					270	
Leu	Thr	Ser	Ser	Leu	Asn	Ser	Ala	Ser	Pro	Val	Ala	Met	Ser		
	275							280					285		
Ser	Ser	Tyr	Asp	Gln	Ser	Ser	Val	His	Asn	Arg	Ile	Pro	Tyr	Gln	
	290							295					300		
Ser	Pro	Val	Ser	Ser	Ser	Glu	Ser	Ala	Pro	Gly	Thr	Ile	Met	Asn	
	305								310					315	
Gly	His	Gly	Gly	Gly	Arg	Ser	Gln	Gln	Thr	Leu	Asp	Ser	Lys	Tyr	
	320								325					330	
Ser	Ser	Lys	Leu	Leu	Leu	Ser	Trp	Leu	Val	Pro	Thr	Lys	Gln	Arg	
	335								340					345	
Lys	Arg	Ile	Ala	His	Val	Met	Trp	Lys	Thr	Pro	Val	Gly	Gln	Trp	
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Leu Ile Arg															

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<210> 73
<211> 26
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-26
<223> Synthetic construct.

<400> 73
 aattcatggc aaatatttcc cttccc 26

<210> 74
<211> 22
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-22
<223> Synthetic construct.

<400> 74
 tggtaaactg gcccaaactc gg 22

<210> 75
<211> 50

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<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-50
<223> Synthetic construct

<400> 75
ttaaagtcat ccgtccttgg ctcaggattt ggagagcttgc accaccaaaa 50

<210> 76
<211> 1989
<212> DNA
<213> Homo sapiens

<400> 76
gccgagtgcc acaaagcctg gggctggcg gggccatgg cgctgccatc 50
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caataaagtc cccatctgat tttaaaaaaaaaaaaaaaaa 1989

<210> 77
<211> 341
<212> PRT
<213> Homo sapiens

<400> 77
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20 25 30
Ala Gly Leu Tyr Thr Cys Asn Leu His His His Tyr Cys His Leu
35 40 45
Tyr Glu Ser Leu Ala Val Arg Leu Glu Val Thr Asp Gly Pro Pro
50 55 60
Ala Thr Pro Ala Tyr Trp Asp Gly Glu Lys Glu Val Leu Ala Val
65 70 75

Ala Arg Gly Ala Pro Ala Leu Leu Thr Cys Val Asn Arg Gly His
 80 85 90
 Val Trp Thr Asp Arg His Val Glu Glu Ala Gln Gln Val Val His
 95 100 105
 Trp Asp Arg Gln Pro Pro Gly Val Pro His Asp Arg Ala Asp Arg
 110 115 120
 Leu Leu Asp Leu Tyr Ala Ser Gly Glu Arg Arg Ala Tyr Gly Pro
 125 130 135
 Leu Phe Leu Arg Asp Arg Val Ala Val Gly Ala Asp Ala Phe Glu
 140 145 150
 Arg Gly Asp Phe Ser Leu Arg Ile Glu Pro Leu Glu Val Ala Asp
 155 160 165
 Glu Gly Thr Tyr Ser Cys His Leu His His His Tyr Cys Gly Leu
 170 175 180
 His Glu Arg Arg Val Phe His Leu Thr Val Ala Glu Pro His Ala
 185 190 195
 Glu Pro Pro Pro Arg Gly Ser Pro Gly Asn Gly Ser Ser His Ser
 200 205 210
 Gly Ala Pro Gly Pro Asp Pro Thr Leu Ala Arg Gly His Asn Val
 215 220 225
 Ile Asn Val Ile Val Pro Glu Ser Arg Ala His Phe Phe Gln Gln
 230 235 240
 Leu Gly Tyr Val Leu Ala Thr Leu Leu Phe Ile Leu Leu Leu
 245 250 255
 Val Thr Val Leu Leu Ala Ala Arg Arg Arg Gly Gly Tyr Glu
 260 265 270
 Tyr Ser Asp Gln Lys Ser Gly Lys Ser Lys Gly Lys Asp Val Asn
 275 280 285
 Leu Ala Glu Phe Ala Val Ala Ala Gly Asp Gln Met Leu Tyr Arg
 290 295 300
 Ser Glu Asp Ile Gln Leu Asp Tyr Lys Asn Asn Ile Leu Lys Glu
 305 310 315
 Arg Ala Glu Leu Ala His Ser Pro Leu Pro Ala Lys Tyr Ile Asp
 320 325 330
 Leu Asp Lys Gly Phe Arg Lys Glu Asn Cys Lys
 335 340

<210> 78

<211> 2243

<212> DNA

<213> Homo sapiens

<400> 78

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<210> 79

<211> 475

<212> PRT

<213> Homo sapiens

<400> 79

Met	Ala	Val	Val	Ser	Glu	Asp	Asp	Phe	Gln	His	Ser	Ser	Asn	Ser
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Thr	Tyr	Gly	Thr	Thr	Ser	Ser	Ser	Leu	Arg	Ala	Asp	Gln	Glu	Ala
														30
20								25						

Leu	Leu	Glu	Lys	Leu	Leu	Asp	Arg	Pro	Pro	Pro	Gly	Leu	Gln	Arg
														45
35								40						

Pro	Glu	Asp	Arg	Phe	Cys	Gly	Thr	Tyr	Ile	Ile	Phe	Phe	Ser	Leu
														60
50								55						

Gly	Ile	Gly	Ser	Leu	Leu	Pro	Trp	Asn	Phe	Phe	Ile	Thr	Ala	Lys
														75
65								70						

Glu	Tyr	Trp	Met	Phe	Lys	Leu	Arg	Asn	Ser	Ser	Ser	Pro	Ala	Thr
														90
80								85						

Gly	Glu	Asp	Pro	Glu	Gly	Ser	Asp	Ile	Leu	Asn	Tyr	Phe	Glu	Ser
														105
95								100						

Tyr Leu Ala Val Ala Ser Thr Val Pro Ser Met Leu Cys Leu Val
 110 115 120
 Ala Asn Phe Leu Leu Val Asn Arg Val Ala Val His Ile Arg Val
 125 130 135
 Leu Ala Ser Leu Thr Val Ile Leu Ala Ile Phe Met Val Ile Thr
 140 145 150
 Ala Leu Val Lys Val Asp Thr Ser Ser Trp Thr Arg Gly Phe Phe
 155 160 165
 Ala Val Thr Ile Val Cys Met Val Ile Leu Ser Gly Ala Ser Thr
 170 175 180
 Val Phe Ser Ser Ser Ile Tyr Gly Met Thr Gly Ser Phe Pro Met
 185 190 195
 Arg Asn Ser Gln Ala Leu Ile Ser Gly Gly Ala Met Gly Gly Thr
 200 205 210
 Val Ser Ala Val Ala Ser Leu Val Asp Leu Ala Ala Ser Ser Asp
 215 220 225
 Val Arg Asn Ser Ala Leu Ala Phe Phe Leu Thr Ala Thr Ile Phe
 230 235 240
 Leu Val Leu Cys Met Gly Leu Tyr Leu Leu Leu Ser Arg Leu Glu
 245 250 255
 Tyr Ala Arg Tyr Tyr Met Arg Pro Val Leu Ala Ala His Val Phe
 260 265 270
 Ser Gly Glu Glu Glu Leu Pro Gln Asp Ser Leu Ser Ala Pro Ser
 275 280 285
 Val Ala Ser Arg Phe Ile Asp Ser His Thr Pro Pro Leu Arg Pro
 290 295 300
 Ile Leu Lys Lys Thr Ala Ser Leu Gly Phe Cys Val Thr Tyr Val
 305 310 315
 Phe Phe Ile Thr Ser Leu Ile Tyr Pro Ala Val Cys Thr Asn Ile
 320 325 330
 Glu Ser Leu Asn Lys Gly Ser Gly Ser Leu Trp Thr Thr Lys Phe
 335 340 345
 Phe Ile Pro Leu Thr Thr Phe Leu Leu Tyr Asn Phe Ala Asp Leu
 350 355 360
 Cys Gly Arg Gln Leu Thr Ala Trp Ile Gln Val Pro Gly Pro Asn
 365 370 375
 Ser Lys Ala Leu Pro Gly Phe Val Leu Leu Arg Thr Cys Leu Ile
 380 385 390
 Pro Leu Phe Val Leu Cys Asn Tyr Gln Pro Arg Val His Leu Lys

395	400	405
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410	415	420
Leu Leu Gly Leu Ser Asn Gly Tyr Leu Ser Thr Leu Ala Leu Leu		
425	430	435
Tyr Gly Pro Lys Ile Val Pro Arg Glu Leu Ala Glu Ala Thr Gly		
440	445	450
Val Val Met Ser Phe Tyr Val Cys Leu Gly Leu Thr Leu Gly Ser		
455	460	465
Ala Cys Ser Thr Leu Leu Val His Leu Ile		
470	475	

<210> 80
<211> 22
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-22
<223> Synthetic construct.

<400> 80
tttgcggtc accattgtct gc 22

<210> 81
<211> 23
<212> DNA
<213> Homo sapiens

<220>
<221> Artificial sequence
<222> 1-23
<223> Synthetic construct.

<400> 81
cgttaggtgac acagaagccc agg 23

<210> 82
<211> 49
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-49
<223> Synthetic construct.

<400> 82
tacggcatga ccggctcctt tcctatgagg aactcccagg cactgatat 49

<210> 83
<211> 1844

<212> DNA
<213> Homo sapiens

<400> 83
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aaggctgaac gcagccaaga cccttcgag aaatgcatgc aggatcctga 200
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cgccgtgtcg ctggcctcgat acacgtggtc ggacgcggcg gcagcgttcg 1300
ccggctttagag ccggaaagag gcgttgcgt tggcgctcga cgacgtggcg 1350

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ggcaaaggaa gaaggcagcc accctccagt ccaaggccag ttatctctcc 1750
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<210> 84

<211> 567

<212> PRT

<213> Homo sapiens

<400> 84

Met	Ala	Pro	Leu	Ala	Leu	His	Leu	Leu	Val	Leu	Val	Pro	Ile	Leu
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Leu	Ser	Leu	Val	Ala	Ser	Gln	Asp	Trp	Lys	Ala	Glu	Arg	Ser	Gln
					20				25				30	
Asp	Pro	Phe	Glu	Lys	Cys	Met	Gln	Asp	Pro	Asp	Tyr	Glu	Gln	Leu
					35				40				45	
Leu	Lys	Val	Val	Thr	Trp	Gly	Leu	Asn	Arg	Thr	Leu	Lys	Pro	Gln
				50					55				60	
Arg	Val	Ile	Val	Val	Gly	Ala	Gly	Val	Ala	Gly	Leu	Val	Ala	Ala
				65				70				75		
Lys	Val	Leu	Ser	Asp	Ala	Gly	His	Lys	Val	Thr	Ile	Leu	Glu	Ala
				80					85				90	
Asp	Asn	Arg	Ile	Gly	Gly	Arg	Ile	Phe	Thr	Tyr	Arg	Asp	Gln	Asn
				95					100				105	
Thr	Gly	Trp	Ile	Gly	Glu	Leu	Gly	Ala	Met	Arg	Met	Pro	Ser	Ser
				110				115				120		
His	Arg	Ile	Leu	His	Lys	Leu	Cys	Gln	Gly	Leu	Gly	Leu	Asn	Leu
				125				130				135		
Thr	Lys	Phe	Thr	Gln	Tyr	Asp	Lys	Asn	Thr	Trp	Thr	Glu	Val	His
				140					145				150	
Glu	Val	Lys	Leu	Arg	Asn	Tyr	Val	Val	Glu	Lys	Val	Pro	Glu	Lys
				155				160				165		

Leu Gly Tyr Ala Leu Arg Pro Gln Glu Lys Gly His Ser Pro Glu
 170 175 180
 Asp Ile Tyr Gln Met Ala Leu Asn Gln Ala Leu Lys Asp Leu Lys
 185 190 195
 Ala Leu Gly Cys Arg Lys Ala Met Lys Lys Phe Glu Arg His Thr
 200 205 210
 Leu Leu Glu Tyr Leu Leu Gly Glu Gly Asn Leu Ser Arg Pro Ala
 215 220 225
 Val Gln Leu Leu Gly Asp Val Met Ser Glu Asp Gly Phe Phe Tyr
 230 235 240
 Leu Ser Phe Ala Glu Ala Leu Arg Ala His Ser Cys Leu Ser Asp
 245 250 255
 Arg Leu Gln Tyr Ser Arg Ile Val Gly Gly Trp Asp Leu Leu Pro
 260 265 270
 Arg Ala Leu Leu Ser Ser Leu Ser Gly Leu Val Leu Leu Asn Ala
 275 280 285
 Pro Val Val Ala Met Thr Gln Gly Pro His Asp Val His Val Gln
 290 295 300
 Ile Glu Thr Ser Pro Pro Ala Arg Asn Leu Lys Val Leu Lys Ala
 305 310 315
 Asp Val Val Leu Leu Thr Ala Ser Gly Pro Ala Val Lys Arg Ile
 320 325 330
 Thr Phe Ser Pro Pro Leu Pro Arg His Met Gln Glu Ala Leu Arg
 335 340 345
 Arg Leu His Tyr Val Pro Ala Thr Lys Val Phe Leu Ser Phe Arg
 350 355 360
 Arg Pro Phe Trp Arg Glu Glu His Ile Glu Gly Gly His Ser Asn
 365 370 375
 Thr Asp Arg Pro Ser Arg Met Ile Phe Tyr Pro Pro Pro Arg Glu
 380 385 390
 Gly Ala Leu Leu Leu Ala Ser Tyr Thr Trp Ser Asp Ala Ala Ala
 395 400 405
 Ala Phe Ala Gly Leu Ser Arg Glu Glu Ala Leu Arg Leu Ala Leu
 410 415 420
 Asp Asp Val Ala Ala Leu His Gly Pro Val Val Arg Gln Leu Trp
 425 430 435
 Asp Gly Thr Gly Val Val Lys Arg Trp Ala Glu Asp Gln His Ser
 440 445 450
 Gln Gly Gly Phe Val Val Gln Pro Pro Ala Leu Trp Gln Thr Glu

455	460	465
Lys Asp Asp Trp Thr Val Pro Tyr Gly Arg Ile Tyr Phe Ala Gly		
470	475	480
Glu His Thr Ala Tyr Pro His Gly Trp Val Glu Thr Ala Val Lys		
485	490	495
Ser Ala Leu Arg Ala Ala Ile Lys Ile Asn Ser Arg Lys Gly Pro		
500	505	510
Ala Ser Asp Thr Ala Ser Pro Glu Gly His Ala Ser Asp Met Glu		
515	520	525
Gly Gln Gly His Val His Gly Val Ala Ser Ser Pro Ser His Asp		
530	535	540
Leu Ala Lys Glu Glu Gly Ser His Pro Pro Val Gln Gly Gln Leu		
545	550	555
Ser Leu Gln Asn Thr Thr His Thr Arg Thr Ser His		
560	565	

<210> 85
 <211> 3316
 <212> DNA
 <213> Homo sapiens

<400> 85
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 tggaggaacc acgagcgagg gaagaaggac agggactcgt gtggcagggaa 150
 gaactcagag ccggaaagcc cccattcact agaagcactg agagatgcgg 200
 ccccctcgca gggctgaaat ttccctgctgc tgttcacaaa gatgctttt 250
 atcttaact ttttggtttc cccacttccg accccggcgt tgatctgcat 300
 cctgacattt ggagctgcca tcttcttgc gctgatcacc agacctcaac 350
 ccgtcttacc tcttcttgc acgttgcgttgg aattgaggaa 400
 ggagcacgga agggggtttc ccagaagaac aatgacctaa caagttgcgt 450
 cttctcagat gccaagacta tgtatgaggt tttccaaaga ggactcgctg 500
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 agatggctat cttacaaaca ggtgtctgat agagcagagt acctgggttc 600
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 tctttgctca gaataggcca gagtggatca tctccaaatt ggcttggcac 700
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 ccgagcctga aggtgatcat ccttatggac cccttgcgt atgacctgaa 900
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 cagctgtgaa gccagagttt gattcttcca agggatatt cggttgctgg 1250
 ctgacgacat gaagactttg aagcccacat tgttccgc ggtgcctcga 1300
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 aaaagggtat catcaggcat gatagtttctt gggacaagct catcttgca 1450
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 gcaccagaga agatagaaaa tatctacaac aggagtcaac cagtgttaca 1950
 aatttttgtt cacggggaga gcttacggtc atccttagta ggagtgggtgg 2000
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ctcttgacac caacattgaa agcaaagcga ggagagctt ccaaatactt 2250
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aactgatctc cccccccctt ggatttagagt tcctgctcta ctttaccac 3250
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tattacagat aaaaaaa 3316

<210> 86
<211> 739
<212> PRT
<213> Homo sapiens

<400> 86
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Gly Lys Lys Asp Arg Asp Ser Cys Gly Arg Lys Asn Ser Glu Pro
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Gly Ser Pro His Ser Leu Glu Ala Leu Arg Asp Ala Ala Pro Ser
 35 40 45
 Gln Gly Leu Asn Phe Leu Leu Phe Thr Lys Met Leu Phe Ile
 50 55 60
 Phe Asn Phe Leu Phe Ser Pro Leu Pro Thr Pro Ala Leu Ile Cys
 65 70 75
 Ile Leu Thr Phe Gly Ala Ala Ile Phe Leu Trp Leu Ile Thr Arg
 80 85 90
 Pro Gln Pro Val Leu Pro Leu Leu Asp Leu Asn Asn Gln Ser Val
 95 100 105
 Gly Ile Glu Gly Gly Ala Arg Lys Gly Val Ser Gln Lys Asn Asn
 110 115 120
 Asp Leu Thr Ser Cys Cys Phe Ser Asp Ala Lys Thr Met Tyr Glu
 125 130 135
 Val Phe Gln Arg Gly Leu Ala Val Ser Asp Asn Gly Pro Cys Leu
 140 145 150
 Gly Tyr Arg Lys Pro Asn Gln Pro Tyr Arg Trp Leu Ser Tyr Lys
 155 160 165
 Gln Val Ser Asp Arg Ala Glu Tyr Leu Gly Ser Cys Leu Leu His
 170 175 180
 Lys Gly Tyr Lys Ser Ser Pro Asp Gln Phe Val Gly Ile Phe Ala
 185 190 195
 Gln Asn Arg Pro Glu Trp Ile Ile Ser Glu Leu Ala Cys Tyr Thr
 200 205 210
 Tyr Ser Met Val Ala Val Pro Leu Tyr Asp Thr Leu Gly Pro Glu
 215 220 225
 Ala Ile Val His Ile Val Asn Lys Ala Asp Ile Ala Met Val Ile
 230 235 240
 Cys Asp Thr Pro Gln Lys Ala Leu Val Leu Ile Gly Asn Val Glu
 245 250 255
 Lys Gly Phe Thr Pro Ser Leu Lys Val Ile Ile Leu Met Asp Pro
 260 265 270
 Phe Asp Asp Asp Leu Lys Gln Arg Gly Glu Lys Ser Gly Ile Glu
 275 280 285
 Ile Leu Ser Leu Tyr Asp Ala Glu Asn Leu Gly Lys Glu His Phe
 290 295 300
 Arg Lys Pro Val Pro Pro Ser Pro Glu Asp Leu Ser Val Ile Cys
 305 310 315
 Phe Thr Ser Gly Thr Gly Asp Pro Lys Gly Ala Met Ile Thr

320	325	330
His Gln Asn Ile Val Ser Asn Ala Ala	Ala Phe Leu Lys Cys Val	
335	340	345
Glu His Ala Tyr Glu Pro Thr Pro Asp	Asp Val Ala Ile Ser Tyr	
350	355	360
Leu Pro Leu Ala His Met Phe Glu Arg	Ile Val Gln Ala Val Val	
365	370	375
Tyr Ser Cys Gly Ala Arg Val Gly Phe	Phe Gln Gly Asp Ile Arg	
380	385	390
Leu Leu Ala Asp Asp Met Lys Thr Leu	Lys Pro Thr Leu Phe Pro	
395	400	405
Ala Val Pro Arg Leu Leu Asn Arg Ile	Tyr Asp Lys Val Gln Asn	
410	415	420
Glu Ala Lys Thr Pro Leu Lys Lys Phe	Leu Leu Lys Leu Ala Val	
425	430	435
Ser Ser Lys Phe Lys Glu Leu Gln Lys	Gly Ile Ile Arg His Asp	
440	445	450
Ser Phe Trp Asp Lys Leu Ile Phe Ala	Lys Ile Gln Asp Ser Leu	
455	460	465
Gly Gly Arg Val Arg Val Ile Val Thr	Gly Ala Ala Pro Met Ser	
470	475	480
Thr Ser Val Met Thr Phe Phe Arg Ala	Ala Met Gly Cys Gln Val	
485	490	495
Tyr Glu Ala Tyr Gly Gln Thr Glu Cys	Thr Gly Gly Cys Thr Phe	
500	505	510
Thr Leu Pro Gly Asp Trp Thr Ser Gly	His Val Gly Val Pro Leu	
515	520	525
Ala Cys Asn Tyr Val Lys Leu Glu Asp	Val Ala Asp Met Asn Tyr	
530	535	540
Phe Thr Val Asn Asn Glu Gly Glu Val	Cys Ile Lys Gly Thr Asn	
545	550	555
Val Phe Lys Gly Tyr Leu Lys Asp Pro	Glu Lys Thr Gln Glu Ala	
560	565	570
Leu Asp Ser Asp Gly Trp Leu His Thr	Gly Asp Ile Gly Arg Trp	
575	580	585
Leu Pro Asn Gly Thr Leu Lys Ile Ile	Asp Arg Lys Lys Asn Ile	
590	595	600
Phe Lys Leu Ala Gln Gly Glu Tyr Ile	Ala Pro Glu Lys Ile Glu	
605	610	615

Asn Ile Tyr Asn Arg Ser Gln Pro Val Leu Gln Ile Phe Val His
 620 625 630
 Gly Glu Ser Leu Arg Ser Ser Leu Val Gly Val Val Val Pro Asp
 635 640 645
 Thr Asp Val Leu Pro Ser Phe Ala Ala Lys Leu Gly Val Lys Gly
 650 655 660
 Ser Phe Glu Glu Leu Cys Gln Asn Gln Val Val Arg Glu Ala Ile
 665 670 675
 Leu Glu Asp Leu Gln Lys Ile Gly Lys Glu Ser Gly Leu Lys Thr
 680 685 690
 Phe Glu Gln Val Lys Ala Ile Phe Leu His Pro Glu Pro Phe Ser
 695 700 705
 Ile Glu Asn Gly Leu Leu Thr Pro Thr Leu Lys Ala Lys Arg Gly
 710 715 720
 Glu Leu Ser Lys Tyr Phe Arg Thr Gln Ile Asp Ser Leu Tyr Glu
 725 730 735
 His Ile Gln Asp

<210> 87
 <211> 2725
 <212> DNA
 <213> Homo sapiens

<400> 87
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 cccctcatca agcccttgg ggctcggaa aagcggagct ggtaccttac 200
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 cagggccgt gctttcctg ctggtgactg tcattgtcaa tatcaagtgg 300
 atcctggaca ctcggcgagc catcagtgaa gccaatgaag acccagagcc 350
 agagcaagac tatgatgagg ccctaggccc cctggagccc ccacggcga 400
 gagggcgtgg tccccggcgg gtcctggacg tagaggtgta ttcaagtcgc 450
 agcaaagtat atgtggcagt ggatggcacc acggtgctgg aggtgagggc 500
 ccgggagcag ggccggggca tccatgtcat tgtcctcaac caggccacgg 550
 gccacgtat ggcaaaacgt gtgtttgaca cgtactcacc tcatgaggat 600
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gacacagagc tgaaccgtcg ccggccggcgc ttctgcagca aagttgaggg 950
ctatgaaatgtatgcagct gcaaggaccc cacacccatc gagttcagcc 1000
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aaaaaaaaaa aaaaaaaaaa aaaaa 2725

<210> 88
<211> 660
<212> PRT
<213> Homo sapiens

<400> 88
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Arg Lys Lys Arg Ser Trp Tyr Leu Thr Trp Lys Tyr Lys Leu Thr
20 25 30
Asn Gln Arg Ala Leu Arg Arg Phe Cys Gln Thr Gly Ala Val Leu
35 40 45
Phe Leu Leu Val Thr Val Ile Val Asn Ile Lys Leu Ile Leu Asp
50 55 60
Thr Arg Arg Ala Ile Ser Glu Ala Asn Glu Asp Pro Glu Pro Glu
65 70 75
Gln Asp Tyr Asp Glu Ala Leu Gly Arg Leu Glu Pro Pro Arg Arg
80 85 90
Arg Gly Ser Gly Pro Arg Arg Val Leu Asp Val Glu Val Tyr Ser
95 100 105
Ser Arg Ser Lys Val Tyr Val Ala Val Asp Gly Thr Thr Val Leu
110 115 120
Glu Asp Glu Ala Arg Glu Gln Gly Arg Gly Ile His Val Ile Val
125 130 135

Leu Asn Gln Ala Thr Gly His Val Met Ala Lys Arg Val Phe Asp
 140 145 150
 Thr Tyr Ser Pro His Glu Asp Glu Ala Met Val Leu Phe Leu Asn
 155 160 165
 Met Val Ala Pro Gly Arg Val Leu Ile Cys Thr Val Lys Asp Glu
 170 175 180
 Gly Ser Phe His Leu Lys Asp Thr Ala Lys Ala Leu Leu Arg Ser
 185 190 195
 Leu Gly Ser Gln Ala Gly Pro Ala Leu Gly Trp Arg Asp Thr Trp
 200 205 210
 Ala Phe Val Gly Arg Lys Gly Gly Pro Val Phe Gly Glu Lys His
 215 220 225
 Ser Lys Ser Pro Ala Leu Ser Ser Trp Gly Asp Pro Val Leu Leu
 230 235 240
 Lys Thr Asp Val Pro Leu Ser Ser Ala Glu Glu Ala Glu Cys His
 245 250 255
 Trp Ala Asp Thr Glu Leu Asn Arg Arg Arg Arg Arg Phe Cys Ser
 260 265 270
 Lys Val Glu Gly Tyr Gly Ser Val Cys Ser Cys Lys Asp Pro Thr
 275 280 285
 Pro Ile Glu Phe Ser Pro Asp Pro Leu Pro Asp Asn Lys Val Leu
 290 295 300
 Asn Val Pro Val Ala Val Ile Ala Gly Asn Arg Pro Asn Tyr Leu
 305 310 315
 Tyr Arg Met Leu Arg Ser Leu Leu Ser Ala Gln Gly Val Ser Pro
 320 325 330
 Gln Met Ile Thr Val Phe Ile Asp Gly Tyr Tyr Glu Glu Pro Met
 335 340 345
 Asp Val Val Ala Leu Phe Gly Leu Arg Gly Ile Gln His Thr Pro
 350 355 360
 Ile Ser Ile Lys Asn Ala Arg Val Ser Gln His Tyr Lys Ala Ser
 365 370 375
 Leu Thr Ala Thr Phe Asn Leu Phe Pro Glu Ala Lys Phe Ala Val
 380 385 390
 Val Leu Glu Glu Asp Leu Asp Ile Ala Val Asp Phe Phe Ser Phe
 395 400 405
 Leu Ser Gln Ser Ile His Leu Leu Glu Glu Asp Asp Ser Leu Tyr
 410 415 420
 Cys Ile Ser Ala Trp Asn Asp Gln Gly Tyr Glu His Thr Ala Glu

425	430	435
Asp Pro Ala Leu Leu Tyr Arg Val Glu	Thr Met Pro Gly Leu Gly	
440	445	450
Trp Val Leu Arg Arg Ser Leu Tyr Lys	Glu Glu Leu Glu Pro Lys	
455	460	465
Trp Pro Thr Pro Glu Lys Leu Trp Asp	Trp Asp Met Trp Met Arg	
470	475	480
Met Pro Glu Gln Arg Arg Gly Arg Glu	Cys Ile Ile Pro Asp Val	
485	490	495
Ser Arg Ser Tyr His Phe Gly Ile Val	Gly Leu Asn Met Asn Gly	
500	505	510
Tyr Phe His Glu Ala Tyr Phe Lys Lys	His Lys Phe Asn Thr Val	
515	520	525
Pro Gly Val Gln Leu Arg Asn Val Asp	Ser Leu Lys Lys Glu Ala	
530	535	540
Tyr Glu Val Glu Val His Arg Leu Leu	Ser Glu Ala Glu Val Leu	
545	550	555
Asp His Ser Lys Asn Pro Cys Glu Asp	Ser Phe Leu Pro Asp Thr	
560	565	570
Glu Gly His Thr Tyr Val Ala Phe Ile	Arg Met Glu Lys Asp Asp	
575	580	585
Asp Phe Thr Thr Trp Thr Gln Leu Ala	Lys Cys Leu His Ile Trp	
590	595	600
Asp Leu Asp Val Arg Gly Asn His Arg	Gly Leu Trp Arg Leu Phe	
605	610	615
Arg Lys Lys Asn His Phe Leu Val Val	Gly Val Pro Ala Ser Pro	
620	625	630
Tyr Ser Val Lys Lys Pro Pro Ser Val	Thr Pro Ile Phe Leu Glu	
635	640	645
Pro Pro Pro Lys Glu Glu Gly Ala Pro	Gly Ala Pro Glu Gln Thr	
650	655	660

<210> 89
 <211> 25
 <212> DNA
 <213> Artificial

<220>
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 <222> 1-25
 <223> Synthetic construct.

<400> 89

gatggcaaaa cgtgtgtttg acacg 25
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<223> Synthetic construct.

<400> 90
cctcaaccag gccacgggcc ac 22

<210> 91
<211> 24
<212> DNA
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<222> 1-24
<223> Synthetic construct.

<400> 91
cccaggcaga gatgcagtagtac aggc 24

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<211> 26
<212> DNA
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<222> 1-26
<223> Synthetic construct.

<400> 92
cctccagtag gtggatggat tggctc 26

<210> 93
<211> 47
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-47
<223> Synthetic construct.

<400> 93
ctcacctcat gaggatgagg ccatggtgct attcctcaac atggtag 47

<210> 94
<211> 3037
<212> DNA
<213> Homo sapiens

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ggatgatttc atctccattt gcctgctgtc tctggctatg ttgggtggat 200
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 ttgtcaaata aatagcagat tgttagtgtca aaaaaaa 3037

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 <211> 307
 <212> PRT
 <213> Homo sapiens

 <400> 95
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 35 40 45
 Leu Cys Gly Thr Ala Leu Ala Val Ile Val Pro Glu Gly Val His
 50 55 60
 Ala Leu Tyr Glu Asp Ile Leu Glu Gly Lys His His Gln Ala Ser
 65 70 75
 Glu Thr His Asn Val Ile Ala Ser Asp Lys Ala Ala Glu Lys Ser
 80 85 90
 Val Val His Glu His Ser His Asp His Thr Gln Leu His
 95 100 105
 Ala Tyr Ile Gly Val Ser Leu Val Leu Gly Phe Val Phe Met Leu
 110 115 120
 Leu Val Asp Gln Ile Gly Asn Ser His Val His Ser Thr Asp Asp
 125 130 135
 Pro Glu Ala Ala Arg Ser Ser Asn Ser Lys Ile Thr Thr Thr Leu
 140 145 150
 Gly Leu Val Val His Ala Ala Ala Asp Gly Val Ala Leu Gly Ala
 155 160 165
 Ala Ala Ser Thr Ser Gln Thr Ser Val Gln Leu Ile Val Phe Val
 170 175 180
 Ala Ile Met Leu His Lys Ala Pro Ala Ala Phe Gly Leu Val Ser
 185 190 195
 Phe Leu Met His Ala Gly Leu Glu Arg Asn Arg Ile Arg Lys His
 200 205 210
 Leu Leu Val Phe Ala Leu Ala Ala Pro Val Met Ser Met Val Thr
 215 220 225
 Tyr Leu Gly Leu Ser Lys Ser Lys Glu Ala Leu Ser Glu Val

230	235	240
Asn Ala Thr Gly Val Ala Met Leu Phe Ser Ala Gly Thr Phe Leu		
245	250	255
Tyr Val Ala Thr Val His Val Leu Pro Glu Val Gly Gly Ile Gly		
260	265	270
His Ser His Lys Pro Asp Ala Thr Gly Gly Arg Gly Leu Ser Arg		
275	280	285
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290	295	300
Leu Ser Val Gly His Gln His		
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<210> 96
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<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-25
<223> Synthetic construct.

<400> 96
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<210> 97
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-25
<223> Synthetic construct.

<400> 97
ctgtgctcat gttcatggac aactg 25

<210> 98
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
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<223> Synthetic construct.

<400> 98
ggatgatttc atctccatta gcctgctgtc tctggctatg ttgggtggat 50

<210> 99
<211> 1429

<212> DNA
<213> Homo sapiens

<400> 99
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 35 40 45
 Ile Met Glu Leu Glu Gly Arg Val Arg Arg Ala Ala Ala Glu Arg
 50 55 60
 Gly Ala Val Glu Leu Lys Lys Asn Glu Phe Gln Gly Glu Leu Glu
 65 70 75
 Lys Gln Arg Glu Gln Leu Asp Lys Ile Gln Ser Ser His Asn Phe
 80 85 90
 Gln Leu Glu Ser Val Asn Lys Leu Tyr Gln Asp Glu Lys Ala Val
 95 100 105
 Leu Val Asn Asn Ile Thr Thr Gly Glu Arg Leu Ile Arg Val Leu
 110 115 120
 Gln Asp Gln Leu Lys Thr Leu Gln Arg Asn Tyr Gly Arg Leu Gln
 125 130 135
 Gln Asp Val Leu Gln Phe Gln Lys Asn Gln Thr Asn Leu Glu Arg
 140 145 150
 Lys Phe Ser Tyr Asp Leu Ser Gln Cys Ile Asn Gln Met Lys Glu
 155 160 165
 Val Lys Glu Gln Cys Glu Glu Arg Ile Glu Glu Val Thr Lys Lys
 170 175 180
 Gly Asn Glu Ala Val Ala Ser Arg Asp Leu Ser Glu Asn Asn Asp
 185 190 195
 Gln Arg Gln Gln Leu Gln Ala Leu Ser Glu Pro Gln Pro Arg Leu
 200 205 210
 Gln Ala Ala Gly Leu Pro His Thr Glu Val Pro Gln Gly Lys Gly
 215 220 225
 Asn Val Leu Gly Asn Ser Lys Ser Gln Thr Pro Ala Pro Ser Ser
 230 235 240

Glu Val Val Leu Asp Ser Lys Arg Gln Val Glu Lys Glu Glu Thr
 245 250 255
 Asn Glu Ile Gln Val Val Asn Glu Glu Pro Gln Arg Asp Arg Leu
 260 265 270
 Pro Gln Glu Pro Gly Arg Glu Gln Val Val Glu Asp Arg Pro Val
 275 280 285
 Gly Gly Arg Gly Phe Gly Gly Ala Gly Glu Leu Gly Gln Thr Pro
 290 295 300
 Gln Val Gln Ala Ala Leu Ser Val Ser Gln Glu Asn Pro Glu Met
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 Glu Gly Pro Glu Arg Asp Gln Leu Val Ile Pro Asp Gly Gln Glu
 320 325 330
 Glu Glu Gln Glu Ala Ala Gly Glu Gly Arg Asn Gln Gln Lys Leu
 335 340 345
 Arg Gly Glu Asp Asp Tyr Asn Met Asp Glu Asn Glu Ala Glu Ser
 350 355 360
 Glu Thr Asp Lys Gln Ala Ala Leu Ala Gly Asn Asp Arg Asn Ile
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 395 400

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 <211> 3671
 <212> DNA
 <213> Homo sapiens

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<211> 1089

<212> PRT

<213> Homo sapiens

<400> 102

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					20				25				30	
Thr	Arg	Leu	Glu	Leu	Thr	Asn	His	Ser	Ser	Cys	Gln	Glu	Pro	Pro
					35				40				45	
Gly	Pro	Gly	Ser	Leu	Pro	Trp	Gly	Ser	Gln	Gly	Lys	Pro	Gly	Ala
					50				55				60	
Cys	Trp	Met	Ala	Ser	Arg	Phe	Ser	Arg	Val	Val	Leu	Val	Leu	Ile
					65				70				75	
Asp	Ala	Leu	Arg	Phe	Asp	Phe	Ala	Gln	Pro	Gln	His	Ser	His	Val
					80				85				90	
Pro	Arg	Glu	Pro	Pro	Val	Ser	Leu	Pro	Phe	Leu	Gly	Lys	Leu	Ser
					95				100				105	
Ser	Leu	Gln	Arg	Ile	Leu	Glu	Ile	Gln	Pro	His	His	Ala	Arg	Leu
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Tyr	Arg	Ser	Gln	Val	Asp	Pro	Pro	Thr	Thr	Thr	Met	Gln	Arg	Leu
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Lys	Ala	Leu	Thr	Thr	Gly	Ser	Leu	Pro	Thr	Phe	Ile	Asp	Ala	Gly
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Ser	Asn	Phe	Ala	Ser	His	Ala	Ile	Val	Glu	Asp	Asn	Leu	Ile	Lys
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Gln	Leu	Thr	Ser	Ala	Gly	Arg	Arg	Val	Val	Phe	Met	Gly	Asp	Asp
					170				175				180	
Thr	Trp	Lys	Asp	Leu	Phe	Pro	Gly	Ala	Phe	Ser	Lys	Ala	Phe	Phe
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Phe	Pro	Ser	Phe	Asn	Val	Arg	Asp	Leu	Asp	Thr	Val	Asp	Asn	Gly

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Ile Leu Glu His Leu Tyr Pro Thr Met Asp Ser Gly Glu Trp Asp		
215	220	225
Val Leu Ile Ala His Phe Leu Gly Val Asp His Cys Gly His Lys		
230	235	240
His Gly Pro His His Pro Glu Met Ala Lys Lys Leu Ser Gln Met		
245	250	255
Asp Gln Val Ile Gln Gly Leu Val Glu Arg Leu Glu Asn Asp Thr		
260	265	270
Leu Leu Val Val Ala Gly Asp His Gly Met Thr Thr Asn Gly Asp		
275	280	285
His Gly Gly Asp Ser Glu Leu Glu Val Ser Ala Ala Leu Phe Leu		
290	295	300
Tyr Ser Pro Thr Ala Val Phe Pro Ser Thr Pro Pro Glu Glu Pro		
305	310	315
Glu Val Ile Pro Gln Val Ser Leu Val Pro Thr Leu Ala Leu Leu		
320	325	330
Leu Gly Leu Pro Ile Pro Phe Gly Asn Ile Gly Glu Val Met Ala		
335	340	345
Glu Leu Phe Ser Gly Gly Glu Asp Ser Gln Pro His Ser Ser Ala		
350	355	360
Leu Ala Gln Ala Ser Ala Leu His Leu Asn Ala Gln Gln Val Ser		
365	370	375
Arg Phe Leu His Thr Tyr Ser Ala Ala Thr Gln Asp Leu Gln Ala		
380	385	390
Lys Glu Leu His Gln Leu Gln Asn Leu Phe Ser Lys Ala Ser Ala		
395	400	405
Asp Tyr Gln Trp Leu Leu Gln Ser Pro Lys Gly Ala Glu Ala Thr		
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425	430	435
Arg Ala Met Cys Ile Glu Ser Trp Ala Arg Phe Ser Leu Val Arg		
440	445	450
Met Ala Gly Gly Thr Ala Leu Leu Ala Ala Ser Cys Phe Ile Cys		
455	460	465
Leu Leu Ala Ser Gln Trp Ala Ile Ser Pro Gly Phe Pro Phe Cys		
470	475	480
Pro Leu Leu Leu Thr Pro Val Ala Trp Gly Leu Val Gly Ala Ile		
485	490	495

Ala Tyr Ala Gly Leu Leu Gly Thr Ile Glu Leu Lys Leu Asp Leu
 500 505 510
 Val Leu Leu Gly Ala Val Ala Val Ser Ser Phe Leu Pro Phe
 515 520 525
 Leu Trp Lys Ala Trp Ala Gly Trp Gly Ser Lys Arg Pro Leu Ala
 530 535 540
 Thr Leu Phe Pro Ile Pro Gly Pro Val Leu Leu Leu Leu Leu Phe
 545 550 555
 Arg Leu Ala Val Phe Phe Ser Asp Ser Phe Val Val Ala Glu Ala
 560 565 570
 Arg Ala Thr Pro Phe Leu Leu Gly Ser Phe Ile Leu Leu Leu Val
 575 580 585
 Val Gln Leu His Trp Glu Gly Gln Leu Leu Pro Pro Lys Leu Leu
 590 595 600
 Thr Met Pro Arg Leu Gly Thr Ser Ala Thr Thr Asn Pro Pro Arg
 605 610 615
 His Asn Gly Ala Tyr Ala Leu Arg Leu Gly Ile Gly Leu Leu Leu
 620 625 630
 Cys Thr Arg Leu Ala Gly Leu Phe His Arg Cys Pro Glu Glu Thr
 635 640 645
 Pro Val Cys His Ser Ser Pro Trp Leu Ser Pro Leu Ala Ser Met
 650 655 660
 Val Gly Gly Arg Ala Lys Asn Leu Trp Tyr Gly Ala Cys Val Ala
 665 670 675
 Ala Leu Val Ala Leu Leu Ala Ala Val Arg Leu Trp Leu Arg Arg
 680 685 690
 Tyr Gly Asn Leu Lys Ser Pro Glu Pro Pro Met Leu Phe Val Arg
 695 700 705
 Trp Gly Leu Pro Leu Met Ala Leu Gly Thr Ala Ala Tyr Trp Ala
 710 715 720
 Leu Ala Ser Gly Ala Asp Glu Ala Pro Pro Arg Leu Arg Val Leu
 725 730 735
 Val Ser Gly Ala Ser Met Val Leu Pro Arg Ala Val Ala Gly Leu
 740 745 750
 Ala Ala Ser Gly Leu Ala Leu Leu Leu Trp Lys Pro Val Thr Val
 755 760 765
 Leu Val Lys Ala Gly Ala Gly Ala Pro Arg Thr Arg Thr Val Leu
 770 775 780
 Thr Pro Phe Ser Gly Pro Pro Thr Ser Gln Ala Asp Leu Asp Tyr

785	790	795
Val Val Pro Gln Ile Tyr Arg His Met	Gln Glu Glu Phe Arg	Gly
800	805	810
Arg Leu Glu Arg Thr Lys Ser Gln Gly	Pro Leu Thr Val Ala Ala	
815	820	825
Tyr Gln Leu Gly Ser Val Tyr Ser Ala	Ala Met Val Thr Ala Leu	
830	835	840
Thr Leu Leu Ala Phe Pro Leu Leu Leu	His Ala Glu Arg Ile	
845	850	855
Ser Leu Val Phe Leu Leu Phe Leu Gln	Ser Phe Leu Leu Leu	
860	865	870
His Leu Leu Ala Ala Gly Ile Pro Val	Thr Thr Pro Gly Pro Phe	
875	880	885
Thr Val Pro Trp Gln Ala Val Ser Ala	Trp Ala Leu Met Ala Thr	
890	895	900
Gln Thr Phe Tyr Ser Thr Gly His Gln	Pro Val Phe Pro Ala Ile	
905	910	915
His Trp His Ala Ala Phe Val Gly Phe	Pro Glu Gly His Gly Ser	
920	925	930
Cys Thr Trp Leu Pro Ala Leu Leu Val	Gly Ala Asn Thr Phe Ala	
935	940	945
Ser His Leu Leu Phe Ala Val Gly Cys	Pro Leu Leu Leu Leu Trp	
950	955	960
Pro Phe Leu Cys Glu Ser Gln Gly Leu	Arg Lys Arg Gln Gln Pro	
965	970	975
Pro Gly Asn Glu Ala Asp Ala Arg Val	Arg Pro Glu Glu Glu Glu	
980	985	990
Glu Pro Leu Met Glu Met Arg Leu Arg	Asp Ala Pro Gln His Phe	
995	1000	1005
Tyr Ala Ala Leu Leu Gln Leu Gly	Leu Lys Tyr Leu Phe Ile Leu	
1010	1015	1020
Gly Ile Gln Ile Leu Ala Cys Ala Leu	Ala Ala Ser Ile Leu Arg	
1025	1030	1035
Arg His Leu Met Val Trp Lys Val Phe	Ala Pro Lys Phe Ile Phe	
1040	1045	1050
Glu Ala Val Gly Phe Ile Val Ser Ser	Val Gly Leu Leu Leu Gly	
1055	1060	1065
Ile Ala Leu Val Met Arg Val Asp Gly	Ala Val Ser Ser Trp Phe	
1070	1075	1080

Arg Gln Leu Phe Leu Ala Gln Gln Arg
1085

<210> 103
<211> 1743
<212> DNA
<213> Homo sapiens

<400> 103
tgccgctgcc gcccgtgctg ctgttgctcc tggccggcgcc ttggggacgg 50
gcaggttccct gtgtctctgg tggtttgccct aaacctgcaa acatcacctt 100
cttatccatc aacatgaaga atgtcctaca atggactcca ccagagggtc 150
ttcaaggagt taaagttact tacactgtgc agtatttcat cacaattgg 200
cccacccagag gtggcactga ctacagatga gaagtccatt tctgttgcc 250
tgacagctcc agagaagtgg aagagaaatc cagaagacct tcctgtttcc 300
atgcaacaaa tatactccaa tctgaagtat aacgtgtctg tggtaatac 350
taaatcaaac agaacgtggt cccagtgtgt gaccaaccac acgctgggtc 400
tcacctggct ggagccgaac actctttact gcgtacacgt ggagtccctc 450
gtccccagggc cccctcgccg tgctcagcct tctgagaagc agtgtgccag 500
gactttgaaa gatcaatcat cagagttcaa ggctaaaatc atcttctgg 550
atgtttgcc catatctatt accgtgttcc tttttctgt gatggctat 600
tccatctacc gatatatcca cggtggcaaa gagaaacacc cagcaaattt 650
gattttgatt tatggaaatg aatttgacaa aagattctt gtgcctgctg 700
aaaaaatcgt gattaacttt atcaccctca atatctcgga tgattctaaa 750
atttctcatc aggatatgag ttactggga aaaagcagtg atgtatccag 800
ccttaatgtat cctcagccca gcgggaacct gaggccccct caggaggaag 850
aggaggtgaa acatttaggg tatgcttcgc atttgatgga aatttttgt 900
gactctgaag aaaacacgga aggtacttct ctcacccagc aagagtccct 950
cagcagaaca atacccccgg ataaaacagt cattgaatat gaatatgatg 1000
tcagaaccac tgacatttgt gcggggcctg aagagcagga gctcagttg 1050
caggaggagg tgtccacaca aggaacatta ttggagtcgc aggcagcgtt 1100
ggcagtcttg ggcccgcaaa cgttacagta ctcatacacc cctcagctcc 1150
aagacttaga cccccctggcg caggagcaca cagactcgga ggagggccg 1200
gaggaagagc catcgacgac cctggtcgac tggatcccc aaactggcag 1250

gctgtgtatt cttcgctgt ccagcttcga ccaggattca gagggtcg 1300
agccttctga gggggatggg ctcggagagg agggtcttct atctagactc 1350
tatgaggagc cggctccaga caggccacca ggagaaaatg aaacctatct 1400
catgcaattc atggaggaat ggggttata tgtgcagatg gaaaactgat 1450
gccaacactt cttttgcct tttgtttctt gtgcaaacaa gtgagtcacc 1500
cctttgatcc cagccataaa gtacctggg tgaaagaagt ttttccagt 1550
ttgtcagtgt ctgtgagaat tacttatttc ttttctctat tctcatagca 1600
cgtgtgtat tggttcatgc atgttaggtct cttaacaatg atggtggcc 1650
tctggagtcc aggggctggc cggttgttct atgcagagaa agcagtcaat 1700
aaatgtttgc cagactgggt gcagaattta ttcaggtggg tgt 1743

<210> 104

<211> 442

<212> PRT

<213> Homo sapiens

<400> 104

Met	Ser	Tyr	Asn	Gly	Leu	His	Gln	Arg	Val	Phe	Lys	Glu	Leu	Lys
1				5					10				15	
Leu	Leu	Thr	Leu	Cys	Ser	Ile	Ser	Ser	Gln	Ile	Gly	Pro	Pro	Glu
				20						25				30
Val	Ala	Leu	Thr	Thr	Asp	Glu	Lys	Ser	Ile	Ser	Val	Val	Leu	Thr
					35				40					45
Ala	Pro	Glu	Lys	Trp	Lys	Arg	Asn	Pro	Glu	Asp	Leu	Pro	Val	Ser
					50				55					60
Met	Gln	Gln	Ile	Tyr	Ser	Asn	Leu	Lys	Tyr	Asn	Val	Ser	Val	Leu
					65				70					75
Asn	Thr	Lys	Ser	Asn	Arg	Thr	Trp	Ser	Gln	Cys	Val	Thr	Asn	His
					80				85					90
Thr	Leu	Val	Leu	Thr	Trp	Leu	Glu	Pro	Asn	Thr	Leu	Tyr	Cys	Val
					95				100					105
His	Val	Glu	Ser	Phe	Val	Pro	Gly	Pro	Pro	Arg	Arg	Ala	Gln	Pro
					110				115					120
Ser	Glu	Lys	Gln	Cys	Ala	Arg	Thr	Leu	Lys	Asp	Gln	Ser	Ser	Glu
					125				130					135
Phe	Lys	Ala	Lys	Ile	Ile	Phe	Trp	Tyr	Val	Leu	Pro	Ile	Ser	Ile
					140				145					150
Thr	Val	Phe	Leu	Phe	Ser	Val	Met	Gly	Tyr	Ser	Ile	Tyr	Arg	Tyr
					155				160					165

Ile His Val Gly Lys Glu Lys His Pro Ala Asn Leu Ile Leu Ile
 170 175 180
 Tyr Gly Asn Glu Phe Asp Lys Arg Phe Phe Val Pro Ala Glu Lys
 185 190 195
 Ile Val Ile Asn Phe Ile Thr Leu Asn Ile Ser Asp Asp Ser Lys
 200 205 210
 Ile Ser His Gln Asp Met Ser Leu Leu Gly Lys Ser Ser Asp Val
 215 220 225
 Ser Ser Leu Asn Asp Pro Gln Pro Ser Gly Asn Leu Arg Pro Pro
 230 235 240
 Gln Glu Glu Glu Glu Val Lys His Leu Gly Tyr Ala Ser His Leu
 245 250 255
 Met Glu Ile Phe Cys Asp Ser Glu Glu Asn Thr Glu Gly Thr Ser
 260 265 270
 Leu Thr Gln Gln Glu Ser Leu Ser Arg Thr Ile Pro Pro Asp Lys
 275 280 285
 Thr Val Ile Glu Tyr Glu Tyr Asp Val Arg Thr Thr Asp Ile Cys
 290 295 300
 Ala Gly Pro Glu Glu Gln Glu Leu Ser Leu Gln Glu Glu Val Ser
 305 310 315
 Thr Gln Gly Thr Leu Leu Glu Ser Gln Ala Ala Leu Ala Val Leu
 320 325 330
 Gly Pro Gln Thr Leu Gln Tyr Ser Tyr Thr Pro Gln Leu Gln Asp
 335 340 345
 Leu Asp Pro Leu Ala Gln Glu His Thr Asp Ser Glu Glu Gly Pro
 350 355 360
 Glu Glu Glu Pro Ser Thr Thr Leu Val Asp Trp Asp Pro Gln Thr
 365 370 375
 Gly Arg Leu Cys Ile Pro Ser Leu Ser Ser Phe Asp Gln Asp Ser
 380 385 390
 Glu Gly Cys Glu Pro Ser Glu Gly Asp Gly Leu Gly Glu Glu Gly
 395 400 405
 Leu Leu Ser Arg Leu Tyr Glu Glu Pro Ala Pro Asp Arg Pro Pro
 410 415 420
 Gly Glu Asn Glu Thr Tyr Leu Met Gln Phe Met Glu Glu Trp Gly
 425 430 435
 Leu Tyr Val Gln Met Glu Asn
 440

<210> 105

<211> 21
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-21
<223> Synthetic construct

<400> 105
cgctgctgct gttgctcctg g 21

<210> 106
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 106
cagtgtgcca ggactttg 18

<210> 107
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 107
agtcgcaggc agcgttgg 18

<210> 108
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 108
ctccctccgag tctgtgtgct cctgc 25

<210> 109
<211> 51
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence

<222> 1-51
<223> Synthetic construct.

<400> 109
ggacgggcag ttccctgtgt ctctggtgtt tgccctaaac ctgcaaacat 50

c 51

<210> 110
<211> 1114
<212> DNA
<213> Homo sapiens

<400> 110
cggacgcgtg ggccggacgcg tggggcggacg cgtgggtctc tgcggggaga 50
cgccagcctg cgtctgccat ggggctcggg ttgaggggct ggggacgtcc 100
tctgctgact gtggccacccg ccctgatgct gcccgtgaag ccccccgcag 150
gctcctgggg ggcccagatc atcgggggcc acgaggtgac ccccccactcc 200
agggcctaca tggcatccgt gcgcttcggg ggccaacatc actgcggagg 250
cttcctgctg cgagcccgct gggtggtctc ggccgcccac tgcttcagcc 300
acagagacccctt ccgcactggc ctgggtggc tggggcggcca cgtcctgagt 350
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gccgctccag gcctgaaatg ttccgtggct gggcccccacg ggaagcctga 1000
tgttcaggggt tgggggtggga cgggcagcgg tggggcacac ccattccaca 1050
tgcaaaggc agaagcaaac ccagtaaaat gttaactgac aaaaaaaaaa 1100

aaaaaaaaaa gaaa 1114

<210> 111

<211> 283

<212> PRT

<213> Homo sapiens

<400> 111

Met Gly Leu Gly Leu Arg Gly Trp Gly Arg Pro Leu Leu Thr Val
1 5 10 15

Ala Thr Ala Leu Met Leu Pro Val Lys Pro Pro Ala Gly Ser Trp
20 25 30

Gly Ala Gln Ile Ile Gly Gly His Glu Val Thr Pro His Ser Arg
35 40 45

Pro Tyr Met Ala Ser Val Arg Phe Gly Gly Gln His His Cys Gly
50 55 60

Gly Phe Leu Leu Arg Ala Arg Trp Val Val Ser Ala Ala His Cys
65 70 75

Phe Ser His Arg Asp Leu Arg Thr Gly Leu Val Val Leu Gly Ala
80 85 90

His Val Leu Ser Thr Ala Glu Pro Thr Gln Gln Val Phe Gly Ile
95 100 105

Asp Ala Leu Thr Thr His Pro Asp Tyr His Pro Met Thr His Ala
110 115 120

Asn Asp Ile Cys Leu Leu Arg Leu Asn Gly Ser Ala Val Leu Gly
125 130 135

Pro Ala Val Gly Leu Leu Arg Leu Pro Gly Arg Arg Ala Arg Pro
140 145 150

Pro Thr Ala Gly Thr Arg Cys Arg Val Ala Gly Trp Gly Phe Val
155 160 165

Ser Asp Phe Glu Glu Leu Pro Pro Gly Leu Met Glu Ala Lys Val
170 175 180

Arg Val Leu Asp Pro Asp Val Cys Asn Ser Ser Trp Lys Gly His
185 190 195

Leu Thr Leu Thr Met Leu Cys Thr Arg Ser Gly Asp Ser His Arg
200 205 210

Arg Gly Phe Cys Ser Ala Asp Ser Gly Gly Pro Leu Val Cys Arg
215 220 225

Asn Arg Ala His Gly Leu Val Ser Phe Ser Gly Leu Trp Cys Gly
230 235 240

Asp Pro Lys Thr Pro Asp Val Tyr Thr Gln Val Ser Ala Phe Val
245 250 255

Ala Trp Ile Trp Asp Val Val Arg Arg Ser Ser Pro Gln Pro Gly
260 265 270

Pro Leu Pro Gly Thr Thr Arg Pro Pro Gly Glu Ala Ala
275 280

<210> 112
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 112
gacgtctgca acagctcctg gaag 24

<210> 113
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 113
cgagaaggaa acgaggccgt gag 23

<210> 114
<211> 44
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-44
<223> Synthetic construct.

<400> 114
tgacacttac catgctctgc acccgccagt gggacagcca caga 44

<210> 115
<211> 1808
<212> DNA
<213> Homo sapiens

<400> 115
gagctaccca ggcggctgggt gtgcagcaag ctccgcgcgg actccggacg 50
cctgacgcct gacgcctgtc cccggcccg catgagccgc tacctgctgc 100
cgctgtcggc gctgggcacg gtagcaggcg ccgcccgtgct gctcaaggac 150
tatgtcaccg gtggggcttg ccccagcaag gccaccatcc ctgggaagac 200

ggtcatcgta acgggcgcca acacaggcat cgggaagcag accgccttgg 250
aactggccag gagaggaggc aacatcatcc tggcctgccc agacatggag 300
aagtgtgagg cggcagcaaa ggacatccgc ggggagaccc tcaatcacca 350
tgtcaacgcc cggcacctgg acttggcttc cctcaagtct atccgagagt 400
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gatgcagttt ggcgttaacc acctgggtca ctttcttgc acaaacttgc 550
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<210> 116
 <211> 331
 <212> PRT
 <213> Homo sapiens

<400> 116

Met	Ser	Arg	Tyr	Leu	Leu	Pro	Leu	Ser	Ala	Leu	Gly	Thr	Val	Ala
1				5				10					15	

Gly	Ala	Ala	Val	Leu	Leu	Lys	Asp	Tyr	Val	Thr	Gly	Gly	Ala	Cys
				20				25					30	

Pro	Ser	Lys	Ala	Thr	Ile	Pro	Gly	Lys	Thr	Val	Ile	Val	Thr	Gly
				35				40					45	

Ala	Asn	Thr	Gly	Ile	Gly	Lys	Gln	Thr	Ala	Leu	Glu	Leu	Ala	Arg
				50				55					60	

Arg	Gly	Gly	Asn	Ile	Ile	Leu	Ala	Cys	Arg	Asp	Met	Glu	Lys	Cys
				65				70					75	

Glu	Ala	Ala	Ala	Lys	Asp	Ile	Arg	Gly	Glu	Thr	Leu	Asn	His	His
				80				85					90	

Val	Asn	Ala	Arg	His	Leu	Asp	Leu	Ala	Ser	Leu	Lys	Ser	Ile	Arg
				95				100					105	

Glu	Phe	Ala	Ala	Lys	Ile	Ile	Glu	Glu	Glu	Glu	Arg	Val	Asp	Ile
				110				115					120	

Leu	Ile	Asn	Asn	Ala	Gly	Val	Met	Arg	Cys	Pro	His	Trp	Thr	Thr
				125				130					135	

Glu	Asp	Gly	Phe	Glu	Met	Gln	Phe	Gly	Val	Asn	His	Leu	Gly	His
				140				145					150	

Phe	Leu	Leu	Thr	Asn	Leu	Leu	Asp	Lys	Leu	Lys	Ala	Ser	Ala	
				155				160					165	

Pro	Ser	Arg	Ile	Ile	Asn	Leu	Ser	Ser	Leu	Ala	His	Val	Ala	Gly
				170				175					180	

His	Ile	Asp	Phe	Asp	Asp	Leu	Asn	Trp	Gln	Thr	Arg	Lys	Tyr	Asn
				185				190					195	

Thr	Lys	Ala	Ala	Tyr	Cys	Gln	Ser	Lys	Leu	Ala	Ile	Val	Leu	Phe
				200				205					210	

Thr	Lys	Glu	Leu	Ser	Arg	Arg	Leu	Gln	Gly	Ser	Gly	Val	Thr	Val
				215				220					225	

Asn Ala Leu His Pro Gly Val Ala Arg Thr Glu Leu Gly Arg His
230 235 240
Thr Gly Ile His Gly Ser Thr Phe Ser Ser Thr Thr Leu Gly Pro
245 250 255
Ile Phe Trp Leu Leu Val Lys Ser Pro Glu Leu Ala Ala Gln Pro
260 265 270
Ser Thr Tyr Leu Ala Val Ala Glu Glu Leu Ala Asp Val Ser Gly
275 280 285
Lys Tyr Phe Asp Gly Leu Lys Gln Lys Ala Pro Ala Pro Glu Ala
290 295 300
Glu Asp Glu Glu Val Ala Arg Arg Leu Trp Ala Glu Ser Ala Arg
305 310 315
Leu Val Gly Leu Glu Ala Pro Ser Val Arg Glu Gln Pro Leu Pro
320 325 330
Arg

<210> 117
<211> 2249
<212> DNA
<213> Homo sapiens

<400> 117
gaagttcgcg agcgctggca tgtggtcctg gggcgccgct ggcggcgctg 50
ctggcggtgc tggcgctcgg gacaggagac ccagaaaggg ctgcggctcg 100
gggcgacacg ttctcggcgc tgaccagcgt ggcgcgcgcc ctggcgcccg 150
agcgcggct gctggggctg ctgaggcggt acctgcgcgg ggaggaggcg 200
cggtcgccgg acctgactag attctacgac aaggtaactt ctttgcattga 250
ggattcaaca acccctgtgg ctaaccctct gcttgcattt actctcatca 300
aacgcctgca gtctgactgg aggaatgtgg tacatagtct ggaggccagt 350
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tccagccttt gaggaccttg agggagcagc aaggccctg atgcggctgc 450
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ttctctcaca gggatgact gcttccaagt tggcaagggtg gcctatgaca 600
tgggggattta ttaccatgcc attccatggc tggaggaggc tgtcagtctc 650
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agatgccttg gatcacttgg cctttgctta tttccgggca ggaaatgtt 750
cgtgtccct cagcctctct cgggagttc ttctctacag cccagataat 800
aagaggatgg ccaggaatgt cttgaaatat gaaaggctct tggcagagag 850
cccccaaccac gtggtagctg aggctgtcat ccagaggccc aatatacccc 900
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cagaaaatta gagaacttgc agaaccatgg ctacagaggt cagtgggtgc 1150
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agcccaagca gggagtgccc ccctcccaga agcataatccc agatgagtgg 2150

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 <210> 118
 <211> 544
 <212> PRT
 <213> Homo sapiens
 <400> 118
 Met Gly Pro Gly Ala Arg Leu Ala Ala Leu Leu Ala Val Leu Ala
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 Leu Gly Thr Gly Asp Pro Glu Arg Ala Ala Ala Arg Gly Asp Thr
 20 25 30
 Phe Ser Ala Leu Thr Ser Val Ala Arg Ala Leu Ala Pro Glu Arg
 35 40 45
 Arg Leu Leu Gly Leu Leu Arg Arg Tyr Leu Arg Gly Glu Glu Ala
 50 55 60
 Arg Leu Arg Asp Leu Thr Arg Phe Tyr Asp Lys Val Leu Ser Leu
 65 70 75
 His Glu Asp Ser Thr Thr Pro Val Ala Asn Pro Leu Leu Ala Phe
 80 85 90
 Thr Leu Ile Lys Arg Leu Gln Ser Asp Trp Arg Asn Val Val His
 95 100 105
 Ser Leu Glu Ala Ser Glu Asn Ile Arg Ala Leu Lys Asp Gly Tyr
 110 115 120
 Glu Lys Val Glu Gln Asp Leu Pro Ala Phe Glu Asp Leu Glu Gly
 125 130 135
 Ala Ala Arg Ala Leu Met Arg Leu Gln Asp Val Tyr Met Leu Asn
 140 145 150
 Val Lys Gly Leu Ala Arg Gly Val Phe Gln Arg Val Thr Gly Ser
 155 160 165
 Ala Ile Thr Asp Leu Tyr Ser Pro Lys Arg Leu Phe Ser Leu Thr
 170 175 180
 Gly Asp Asp Cys Phe Gln Val Gly Lys Val Ala Tyr Asp Met Gly
 185 190 195
 Asp Tyr Tyr His Ala Ile Pro Trp Leu Glu Glu Ala Val Ser Leu
 200 205 210
 Phe Arg Gly Ser Tyr Gly Glu Trp Lys Thr Glu Asp Glu Ala Ser
 215 220 225
 Leu Glu Asp Ala Leu Asp His Leu Ala Phe Ala Tyr Phe Arg Ala
 230 235 240

Gly Asn Val Ser Cys Ala Leu Ser Leu Ser Arg Glu Phe Leu Leu
 245 250 255
 Tyr Ser Pro Asp Asn Lys Arg Met Ala Arg Asn Val Leu Lys Tyr
 260 265 270
 Glu Arg Leu Leu Ala Glu Ser Pro Asn His Val Val Ala Glu Ala
 275 280 285
 Val Ile Gln Arg Pro Asn Ile Pro His Leu Gln Thr Arg Asp Thr
 290 295 300
 Tyr Glu Gly Leu Cys Gln Thr Leu Gly Ser Gln Pro Thr Leu Tyr
 305 310 315
 Gln Ile Pro Ser Leu Tyr Cys Ser Tyr Glu Thr Asn Ser Asn Ala
 320 325 330
 Tyr Leu Leu Leu Gln Pro Ile Arg Lys Glu Val Ile His Leu Glu
 335 340 345
 Pro Tyr Ile Ala Leu Tyr His Asp Phe Val Ser Asp Ser Glu Ala
 350 355 360
 Gln Lys Ile Arg Glu Leu Ala Glu Pro Trp Leu Gln Arg Ser Val
 365 370 375
 Val Ala Ser Gly Glu Lys Gln Leu Gln Val Glu Tyr Arg Ile Ser
 380 385 390
 Lys Ser Ala Trp Leu Lys Asp Thr Val Asp Pro Lys Leu Val Thr
 395 400 405
 Leu Asn His Arg Ile Ala Ala Leu Thr Gly Leu Asp Val Arg Pro
 410 415 420
 Pro Tyr Ala Glu Tyr Leu Gln Val Val Asn Tyr Gly Ile Gly Gly
 425 430 435
 His Tyr Glu Pro His Phe Asp His Ala Thr Ser Pro Ser Ser Pro
 440 445 450
 Leu Tyr Arg Met Lys Ser Gly Asn Arg Val Ala Thr Phe Met Ile
 455 460 465
 Tyr Leu Ser Ser Val Glu Ala Gly Gly Ala Thr Ala Phe Ile Tyr
 470 475 480
 Ala Asn Leu Ser Val Pro Val Val Arg Asn Ala Ala Leu Phe Trp
 485 490 495
 Trp Asn Leu His Arg Ser Gly Glu Gly Asp Ser Asp Thr Leu His
 500 505 510
 Ala Gly Cys Pro Val Leu Val Gly Asp Lys Trp Val Ala Asn Lys
 515 520 525
 Trp Ile His Glu Tyr Gly Gln Glu Phe Arg Arg Pro Cys Ser Ser

cgcgggact cggagcaggt gcgctactgc gcgcgttct cctacctctg 250
gctcaagttt tcacttatca tctattccac cgtgttctgg ctgattgggg 300
ccctggtcct gtctgtggc atctatgcag aggttgagcg gcagaaatat 350
aaaacccttg aaagtgcctt cctggctcca gccatcatcc tcatcctct 400
gggcgtcgtc atgttcatgg tctccttcat tggtgtgctg gcgtccctcc 450
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ctcatcatgg agctcattgg tggcgtggg gccttgacct tccggAACCA 550
gaccattgac ttccctgaacg acaacattcg aagaggaatt gagaactact 600
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aagtgtgtg gcggggagga ctaccgagat tggagcaaga atcagtagcca 700
cgactgcagt gcccctggac ccctggctg tgggtgccc tacacctgct 750
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gcatcctcct gggcatcctg cttccccagt tcctgggggt gctgctgacg 950
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ctcttctcag cctccctagg gccttgagcc ctcttgcaag ggcggctgct 1600
tccttgagcc tagttttttt ttacgtgatt tttgtAACAT tcattttttt 1650

gtacagataa caggagtttc tgactaatca aagctggtat ttcccccgc 1700
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catgtttgt tttgtttta aaaaaaaaa 1778

<210> 123
<211> 294
<212> PRT
<213> Homo sapiens

<400> 123
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Ser Tyr Leu Trp Leu Lys Phe Ser Leu Ile Ile Tyr Ser Thr Val
20 25 30
Phe Trp Leu Ile Gly Ala Leu Val Leu Ser Val Gly Ile Tyr Ala
35 40 45
Glu Val Glu Arg Gln Lys Tyr Lys Thr Leu Glu Ser Ala Phe Leu
50 55 60
Ala Pro Ala Ile Ile Leu Ile Leu Gly Val Val Met Phe Met
65 70 75
Val Ser Phe Ile Gly Val Leu Ala Ser Leu Arg Asp Asn Leu Tyr
80 85 90
Leu Leu Gln Ala Phe Met Tyr Ile Leu Gly Ile Cys Leu Ile Met
95 100 105
Glu Leu Ile Gly Gly Val Val Ala Leu Thr Phe Arg Asn Gln Thr
110 115 120
Ile Asp Phe Leu Asn Asp Asn Ile Arg Arg Gly Ile Glu Asn Tyr
125 130 135
Tyr Asp Asp Leu Asp Phe Lys Asn Ile Met Asp Phe Val Gln Lys
140 145 150
Lys Phe Lys Cys Cys Gly Gly Glu Asp Tyr Arg Asp Trp Ser Lys
155 160 165
Asn Gln Tyr His Asp Cys Ser Ala Pro Gly Pro Leu Ala Cys Gly
170 175 180
Val Pro Tyr Thr Cys Cys Ile Arg Asn Thr Thr Glu Val Val Asn
185 190 195
Thr Met Cys Gly Tyr Lys Thr Ile Asp Lys Glu Arg Phe Ser Val
200 205 210
Gln Asp Val Ile Tyr Val Arg Gly Cys Thr Asn Ala Val Ile Ile
215 220 225
Trp Phe Met Asp Asn Tyr Thr Ile Met Ala Cys Ile Leu Leu Gly

230	235	240
Ile Leu Leu Pro Gln Phe Leu Gly Val	Leu Leu Thr Leu Leu Tyr	
245	250	255
Ile Thr Arg Val Glu Asp Ile Ile Met	Glu His Ser Val Thr Asp	
260	265	270
Gly Leu Leu Gly Pro Gly Ala Lys Pro Ser Val Glu Ala Ala Gly		
275	280	285
Thr Gly Cys Cys Leu Cys Tyr Pro Asn		
290		

<210> 124
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 124
atcatctatt ccaccgtgtt ctggc 25

<210> 125
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 125
gacagagtgc tccatgatga tgtcc 25

<210> 126
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 126
cctgtctgtg ggcatctatg cagaggttga gcggcagaaa tataaaaccc 50

<210> 127
<211> 1636
<212> DNA
<213> Homo sapiens

<400> 127
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ctctgtggtt tgctggcagc caccttgcac caagccaccc tcagtcaccc 150
tgcaaggttctc atcctcggcc caaaagtcat caaagaaaag ctgacacagg 200
agctgaagga ccacaacgcc accagcatcc tgcaaggact gcccgtgctc 250
agtgcacatgc gggaaaagcc agccggaggc atccctgtgc tggcagccct 300
ggtgaacacc gtcctgaagc acatcatctg gctgaaggtc atcacagcta 350
acatcctcca gctgcaggtg aagccctcg 400
gtcaagatcc ccctggacat ggtggctgga ttcaacacgc ccctggtaa 450
gaccatcgtg gagttccaca tgacgactga ggcccaagcc accatccqca 500
tggacaccag tgcaagtggc cccacccgccc tggctcttag tgactgtgcc 550
accagccatg ggagcctgctg catccaactg ctgtataaagc ttccttcct 600
ggtgaacgc 650
ccaatcttagt gaaaaaccag ctgtgtcccg tgatcgaggc ttccttcaat 700
ggcatgtatg cagacccctgc gtagctggtg aaggtgccc tttccctcag 750
cattgaccgt ctggagtttgc accttctgtt tcctgccatc aagggtgaca 800
ccattcagct ctacctgggg gccaagttgt tggactcaca gggaaagggtg 850
accaagtggt tcaataactc tgcaaggcttcc ctgacaatgc ccaccctgga 900
caacatcccg ttcagccctca tcgtgagtca ggacgtggtg aaagctgcag 950
tggctgctgt gctctctcca gaagaattca tggctctgtt ggactctgtg 1000
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atgaactctg ggattggctg gttccaaacct gatgttctga aaaacatcat 1350
cactgagatc atccactcca tcctgctgcc gaaccagaat gcacaattaa 1400
gatctgggggt cccagtgta ttggtaagg ccttgggatt cgaggcagct 1450

gagtcctcac tgaccaagga tgcccttgcg cttactccag ccccttgcg 1500
gaaaccgcg tccctgtct cccagtgaag acttggatgg cagccatcg 1550
ggaggctgg gtcccagctg ggagtatgg tggatgtct atagaccatc 1600
cctctctgca atcaataaac acttgcctgt gaaaaa 1636

<210> 128
<211> 484
<212> PRT
<213> Homo sapiens

<400> 128

Met	Ala	Gly	Pro	Trp	Thr	Phe	Thr	Leu	Leu	Cys	Gly	Leu	Leu	Ala
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Ala	Thr	Leu	Ile	Gln	Ala	Thr	Leu	Ser	Pro	Thr	Ala	Val	Leu	Ile
		20						25						30
Leu	Gly	Pro	Lys	Val	Ile	Lys	Glu	Lys	Leu	Thr	Gln	Glu	Leu	Lys
			35					40						45
Asp	His	Asn	Ala	Thr	Ser	Ile	Leu	Gln	Gln	Leu	Pro	Leu	Leu	Ser
				50				55						60
Ala	Met	Arg	Glu	Lys	Pro	Ala	Gly	Gly	Ile	Pro	Val	Leu	Gly	Ser
				65				70						75
Leu	Val	Asn	Thr	Val	Leu	Lys	His	Ile	Ile	Trp	Leu	Lys	Val	Ile
				80				85						90
Thr	Ala	Asn	Ile	Leu	Gln	Leu	Gln	Val	Lys	Pro	Ser	Ala	Asn	Asp
				95				100						105
Gln	Glu	Leu	Leu	Val	Lys	Ile	Pro	Leu	Asp	Met	Val	Ala	Gly	Phe
				110				115						120
Asn	Thr	Pro	Leu	Val	Lys	Thr	Ile	Val	Glu	Phe	His	Met	Thr	Thr
				125				130						135
Glu	Ala	Gln	Ala	Thr	Ile	Arg	Met	Asp	Thr	Ser	Ala	Ser	Gly	Pro
				140				145						150
Thr	Arg	Leu	Val	Leu	Ser	Asp	Cys	Ala	Thr	Ser	His	Gly	Ser	Leu
				155				160						165
Arg	Ile	Gln	Leu	Leu	Tyr	Lys	Leu	Ser	Phe	Leu	Val	Asn	Ala	Leu
				170				175						180
Ala	Lys	Gln	Val	Met	Asn	Leu	Leu	Val	Pro	Ser	Leu	Pro	Asn	Leu
				185				190						195
Val	Lys	Asn	Gln	Leu	Cys	Pro	Val	Ile	Glu	Ala	Ser	Phe	Asn	Gly
				200				205						210
Met	Tyr	Ala	Asp	Leu	Leu	Gln	Leu	Val	Lys	Val	Pro	Ile	Ser	Leu
				215				220						225

Ser Ile Asp Arg Leu Glu Phe Asp Leu Leu Tyr Pro Ala Ile Lys
 230 235 240
 Gly Asp Thr Ile Gln Leu Tyr Leu Gly Ala Lys Leu Leu Asp Ser
 245 250 255
 Gln Gly Lys Val Thr Lys Trp Phe Asn Asn Ser Ala Ala Ser Leu
 260 265 270
 Thr Met Pro Thr Leu Asp Asn Ile Pro Phe Ser Leu Ile Val Ser
 275 280 285
 Gln Asp Val Val Lys Ala Ala Val Ala Val Leu Ser Pro Glu
 290 295 300
 Glu Phe Met Val Leu Leu Asp Ser Val Leu Pro Glu Ser Ala His
 305 310 315
 Arg Leu Lys Ser Ser Ile Gly Leu Ile Asn Glu Lys Ala Ala Asp
 320 325 330
 Lys Leu Gly Ser Thr Gln Ile Val Lys Ile Leu Thr Gln Asp Thr
 335 340 345
 Pro Glu Phe Phe Ile Asp Gln Gly His Ala Lys Val Ala Gln Leu
 350 355 360
 Ile Val Leu Glu Val Phe Pro Ser Ser Glu Ala Leu Arg Pro Leu
 365 370 375
 Phe Thr Leu Gly Ile Glu Ala Ser Ser Glu Ala Gln Phe Tyr Thr
 380 385 390
 Lys Gly Asp Gln Leu Ile Leu Asn Leu Asn Asn Ile Ser Ser Asp
 395 400 405
 Arg Ile Gln Leu Met Asn Ser Gly Ile Gly Trp Phe Gln Pro Asp
 410 415 420
 Val Leu Lys Asn Ile Ile Thr Glu Ile Ile His Ser Ile Leu Leu
 425 430 435
 Pro Asn Gln Asn Gly Lys Leu Arg Ser Gly Val Pro Val Ser Leu
 440 445 450
 Val Lys Ala Leu Gly Phe Glu Ala Ala Glu Ser Ser Leu Thr Lys
 455 460 465
 Asp Ala Leu Val Leu Thr Pro Ala Ser Leu Trp Lys Pro Ser Ser
 470 475 480
 Pro Val Ser Gln

<210> 129
 <211> 2213
 <212> DNA
 <213> Homo sapiens

<400> 129
gagcgaacat ggcagcgcgt tggcggtttt ggtgtgtctc tgtgaccatg 50
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aaagaaggag atgggtttat ctgaaaaggt tagtcagctg atggaatgga 150
ctaacaaaag acctgtaata agaatgaatg gagacaagtt ccgtcgccct 200
gtgaaagccc caccgagaaa ttactccgtt atcgtcatgt tcactgctct 250
ccaaactgcat agacagtgtg tcgtttgc当地 gcaagctgat gaagaattcc 300
agatcctggc aaactcctgg cgatactcca gtgcattcac caacaggata 350
tttttgcca tggtgattt tcatgaaggc tctgatgtat ttcatgatgct 400
aaacatgaat tcaagctccaa ctttcatcaa ctttcctgca aaaggaaac 450
ccaaacgggg tgatacatat gagttacagg tgcggggttt ttcatgatgag 500
cagattgccg ggtggatcgc cgacagaact gatgtcaata ttagagtgtat 550
tagaccccca aattatgctg gtccccttat gttgggattt ctttggctg 600
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aataaaaactg gatgggcttt tgcagcttg tgtttgc当地 ttcatgac 700
atctggtcaa atgtgaaacc atataagagg accaccatat gcccataaga 750
atccccacac gggacatgtg aattatatcc atggaagcag tcaagcccag 800
ttttagctg aaacacacat ttttcttctg ttatgggtg gagttacatt 850
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ctttctgatg agttaaaaag gtcccagaga tatatagaca ctggagtact 1050
ggaaattgaa aaacgaaaat cgtgtgtgt tgaaaagaag aatgcaactt 1100
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ctgaggtatt tgaaaataat tatcctctt accttctctt cccagtgaac 1250
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aactactact ttgttttagt tagaacaaag ctcaaaaacta cttagttaa 1350
cttggtcatac tgatttata ttgccttata caaagatggg gaaagtaagt 1400
cctgaccagg tgttccacata tatgcctgtt acagataact acattaggaa 1450

ttcattctta gcttcttcat ctttgtgtgg atgtgtatac tttacgcata 1500
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gaacaccatt cttcagagca cacgtctagc cctcagcaag acagttgttt 1600
ctcctcctcc ttgcataattt cctactgcgc tccagcctga gtgatagagt 1650
gagactctgt ctcaaaaaaa agtatctcta aatacaggat tataatttct 1700
gcttgagttat ggtgttaact accttgttatt tagaaagatt tcagattcat 1750
tccatctcct tagtttctt ttaaggtgac ccatctgtga taaaaatata 1800
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aaatttagagt ttgtcactta ttccatttgtt acctaagaga aaaataggct 1900
cagttagaaa aggactccct gcccaggcgc agtgaattac gcctgtaatc 1950
tcagcacttt gggaggccaa ggcaggcaga tcacgaggc aggagttcga 2000
gaccatcctg gccaacatgg tgaaaccccg tctctactaa aaatataaaa 2050
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tgaggcacga gaatcacttg aactcaggag atggaggtt cagtgagccg 2150
agatcacgccc actgcactcc agcctggcaa cagagcgaga ctccatctca 2200
aaaaaaaaaa aaa 2213

<210> 130
<211> 335
<212> PRT
<213> Homo sapiens

<400> 130
Met Ala Ala Arg Trp Arg Phe Trp Cys Val Ser Val Thr Met Val
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Val Ala Leu Leu Ile Val Cys Asp Val Pro Ser Ala Ser Ala Gln
20 25 30
Arg Lys Lys Glu Met Val Leu Ser Glu Lys Val Ser Gln Leu Met
35 40 45
Glu Trp Thr Asn Lys Arg Pro Val Ile Arg Met Asn Gly Asp Lys
50 55 60
Phe Arg Arg Leu Val Lys Ala Pro Pro Arg Asn Tyr Ser Val Ile
65 70 75
Val Met Phe Thr Ala Leu Gln Leu His Arg Gln Cys Val Val Cys
80 85 90
Lys Gln Ala Asp Glu Glu Phe Gln Ile Leu Ala Asn Ser Trp Arg
95 100 105

Tyr Ser Ser Ala Phe Thr Asn Arg Ile Phe Phe Ala Met Val Asp
 110 115 120
 Phe Asp Glu Gly Ser Asp Val Phe Gln Met Leu Asn Met Asn Ser
 125 130 135
 Ala Pro Thr Phe Ile Asn Phe Pro Ala Lys Gly Lys Pro Lys Arg
 140 145 150
 Gly Asp Thr Tyr Glu Leu Gln Val Arg Gly Phe Ser Ala Glu Gln
 155 160 165
 Ile Ala Arg Trp Ile Ala Asp Arg Thr Asp Val Asn Ile Arg Val
 170 175 180
 Ile Arg Pro Pro Asn Tyr Ala Gly Pro Leu Met Leu Gly Leu Leu
 185 190 195
 Leu Ala Val Ile Gly Gly Leu Val Tyr Leu Arg Arg Ser Asn Met
 200 205 210
 Glu Phe Leu Phe Asn Lys Thr Gly Trp Ala Phe Ala Ala Leu Cys
 215 220 225
 Phe Val Leu Ala Met Thr Ser Gly Gln Met Trp Asn His Ile Arg
 230 235 240
 Gly Pro Pro Tyr Ala His Lys Asn Pro His Thr Gly His Val Asn
 245 250 255
 Tyr Ile His Gly Ser Ser Gln Ala Gln Phe Val Ala Glu Thr His
 260 265 270
 Ile Val Leu Leu Phe Asn Gly Gly Val Thr Leu Gly Met Val Leu
 275 280 285
 Leu Cys Glu Ala Ala Thr Ser Asp Met Asp Ile Gly Lys Arg Lys
 290 295 300
 Ile Met Cys Val Ala Gly Ile Gly Leu Val Val Leu Phe Phe Ser
 305 310 315
 Trp Met Leu Ser Ile Phe Arg Ser Lys Tyr His Gly Tyr Pro Tyr
 320 325 330
 Ser Phe Leu Met Ser
 335

<210> 131
 <211> 2476
 <212> DNA
 <213> Homo sapiens

<400> 131
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 ctgcttaggga gagaacgcca gagggaggcg gctggcccg gggcaggctc 100

tcagaaccgc taccggcgat gctactgctg tgggtgtcgg tggtcgcagc 150
cttggcgctg gcggtaactgg ccccccggagc aggggagcag aggcggagag 200
cagccaaagc gcccaatgtg gtgctggtcg tgagcgactc ctgcgatgga 250
aggtaacat ttcatccagg aagtcaggtt gtgaaacttc cttttatcaa 300
ctttatgaag acacgtggga ctccctttct gaatgcctac acaaactctc 350
caatttggta cccatcacgc gcagcaatgtt ggagtggcct ctgcactcac 400
ttaacagaat ctggaataa tttaagggtt ctagatccaa attatacaac 450
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aactggacta tacttcagga catcactcca ttagtaatcg tggaaagcg 550
tggacaagag atgttgctt ctactcaga caagaaggca ggcggatgg 600
taatcttatac cgtaacagga ctaaagttagt agttagtgaa agggattggc 650
agaatacaga caaaggcagta aactggtaa gaaaggaagc aattaattac 700
actgaaccat ttgttattta ctgggatata aatttaccac acccttaccc 750
ttcaccatct tctggagaaa attttggatc ttcaacattt cacacatctc 800
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tcacctttgtt cagaaatgca ccctgttagat tattactctt ctatacaaa 900
aaactgcact ggaagattta caaaaaaaga aattaagaat attagagcat 950
tttattatgc tatgtgtgct gagacagatg ccatgcttgg tggaaatttt 1000
ttggcccttc atcaatttgc tcttcttcag aaaactatttgc tcatataactc 1050
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gcatgtacga ggcttagtgca catgttccgc ttttgatgtat gggaccagga 1150
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cccttaccatg cttgatatttgc ctggatttcc tctgccttcag aacctgagtg 1250
gatactctt gttgccgttca tcatcagaaa catttaagaa tgaacataaa 1300
gtcaaaaacc tgcattccacc ctggattctg agtgaatttcc atggatgtaa 1350
tgtgaatgcc tccaccatca tgcttcgaac taaccactgg aaatataatag 1400
cctattcggta tggtgcatca atattgcctc aactctttga tctttcctcg 1450
gatccagatg aattaacaaa tggtgctgtt aaatttccag aaattactta 1500
ttctttggat cagaagcttc attccattat aaactaccct aaagtttctg 1550

cttctgtcca ccagtataat aaagagcagt ttatcaagtg gaaacaaga 1600
ataggacaga attattcaaa cgttatacgca aatcttaggt ggcaccaaga 1650
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aagagattga gaccatcctg gccaacatgg tgaaaccctg tctctactaa 1950
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tattttgtaa gaatgttagt tattttaga taaaatgcca atgattataa 2200
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aaaaaaaaaaa aaaaaaaaaaaa aaaaaaa 2476

<210> 132
<211> 536
<212> PRT
<213> Homo sapiens

<400> 132
Met Leu Leu Leu Trp Val Ser Val Val Ala Ala Leu Ala Leu Ala
1 5 10 15
Val Leu Ala Pro Gly Ala Gly Glu Gln Arg Arg Arg Ala Ala Lys
20 25 30
Ala Pro Asn Val Val Leu Val Val Ser Asp Ser Phe Asp Gly Arg
35 40 45
Leu Thr Phe His Pro Gly Ser Gln Val Val Lys Leu Pro Phe Ile
50 55 60
Asn Phe Met Lys Thr Arg Gly Thr Ser Phe Leu Asn Ala Tyr Thr
65 70 75

Asn Ser Pro Ile Cys Cys Pro Ser Arg Ala Ala Met Trp Ser Gly
 80 85 90
 Leu Phe Thr His Leu Thr Glu Ser Trp Asn Asn Phe Lys Gly Leu
 95 100 105
 Asp Pro Asn Tyr Thr Trp Met Asp Val Met Glu Arg His Gly
 110 115 120
 Tyr Arg Thr Gln Lys Phe Gly Lys Leu Asp Tyr Thr Ser Gly His
 125 130 135
 His Ser Ile Ser Asn Arg Val Glu Ala Trp Thr Arg Asp Val Ala
 140 145 150
 Phe Leu Leu Arg Gln Glu Gly Arg Pro Met Val Asn Leu Ile Arg
 155 160 165
 Asn Arg Thr Lys Val Arg Val Met Glu Arg Asp Trp Gln Asn Thr
 170 175 180
 Asp Lys Ala Val Asn Trp Leu Arg Lys Glu Ala Ile Asn Tyr Thr
 185 190 195
 Glu Pro Phe Val Ile Tyr Leu Gly Leu Asn Leu Pro His Pro Tyr
 200 205 210
 Pro Ser Pro Ser Ser Gly Glu Asn Phe Gly Ser Ser Thr Phe His
 215 220 225
 Thr Ser Leu Tyr Trp Leu Glu Lys Val Ser His Asp Ala Ile Lys
 230 235 240
 Ile Pro Lys Trp Ser Pro Leu Ser Glu Met His Pro Val Asp Tyr
 245 250 255
 Tyr Ser Ser Tyr Thr Lys Asn Cys Thr Gly Arg Phe Thr Lys Lys
 260 265 270
 Glu Ile Lys Asn Ile Arg Ala Phe Tyr Tyr Ala Met Cys Ala Glu
 275 280 285
 Thr Asp Ala Met Leu Gly Glu Ile Ile Leu Ala Leu His Gln Leu
 290 295 300
 Asp Leu Leu Gln Lys Thr Ile Val Ile Tyr Ser Ser Asp His Gly
 305 310 315
 Glu Leu Ala Met Glu His Arg Gln Phe Tyr Lys Met Ser Met Tyr
 320 325 330
 Glu Ala Ser Ala His Val Pro Leu Leu Met Met Gly Pro Gly Ile
 335 340 345
 Lys Ala Gly Leu Gln Val Ser Asn Val Val Ser Leu Val Asp Ile
 350 355 360
 Tyr Pro Thr Met Leu Asp Ile Ala Gly Ile Pro Leu Pro Gln Asn

365	370	375
Leu Ser Gly Tyr Ser Leu Leu Pro Leu	Ser Ser Glu Thr Phe Lys	
380	385	390
Asn Glu His Lys Val Lys Asn Leu His	Pro Pro Trp Ile Leu Ser	
395	400	405
Glu Phe His Gly Cys Asn Val Asn Ala	Ser Thr Tyr Met Leu Arg	
410	415	420
Thr Asn His Trp Lys Tyr Ile Ala Tyr	Ser Asp Gly Ala Ser Ile	
425	430	435
Leu Pro Gln Leu Phe Asp Leu Ser Ser	Asp Pro Asp Glu Leu Thr	
440	445	450
Asn Val Ala Val Lys Phe Pro Glu Ile	Thr Tyr Ser Leu Asp Gln	
455	460	465
Lys Leu His Ser Ile Ile Asn Tyr Pro	Lys Val Ser Ala Ser Val	
470	475	480
His Gln Tyr Asn Lys Glu Gln Phe Ile	Lys Trp Lys Gln Ser Ile	
485	490	495
Gly Gln Asn Tyr Ser Asn Val Ile Ala	Asn Leu Arg Trp His Gln	
500	505	510
Asp Trp Gln Lys Glu Pro Arg Lys Tyr	Glu Asn Ala Ile Asp Gln	
515	520	525
Trp Leu Lys Thr His Met Asn Pro Arg	Ala Val	
530	535	

<210> 133
 <211> 1475
 <212> DNA
 <213> Homo sapiens

<400> 133
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 tcaaggagca agagttcag cctgaagaca agggagcagt ccctgaagac 100
 gcttctactg agaggtctgc catggcctct cttggcctcc aacttgtgg 150
 ctacatccta ggccttctgg ggctttggg cacactggtt gccatgctgc 200
 tccccagctg gaaaacaagt tcttatgtcg gtgccagcat tgtgacagca 250
 gttggcttct ccaaggcct ctggatggaa tgtgccacac acagcacagg 300
 catcacccag tgtgacatct atagcaccct tctggcctg cccgctgaca 350
 tccaggctgc ccaggccatg atggtgacat ccagtgcaat ctcctccctg 400
 gcctgcatta tctctgtggt gggcatgaga tgcacagtct tctgccagga 450

atcccggacc aaagacagag tggcggttagc aggtggagtc tttttcatcc 500
ttggaggcct cctgggattc attcctgttg cctggaatct tcataggatc 550
ctacgggact tctactcacc actgggtcct gacagcatga aatttgagat 600
tggagaggct cttaacttgg gcattatttc ttccctgttc tccctgata 650
ctggaaatcat cctctgcttt tcctgctcat cccagagaaa tcgctccaac 700
tactacgatg cctaccaagc ccaacctttt gccacaagga gctctccaag 750
gcctggtcaa cctcccaaag tcaagagtga gttcaattcc tacagcctga 800
cagggtatgt gtgaagaacc agggggcaga gctgggggtt ggctgggtct 850
gtgaaaaaca gtggacagca ccccgaggc cacaggtgag ggacactacc 900
actggatcgt gtcagaaggt gctgctgagg atagactgac tttggccatt 950
ggattgagca aaggcagaaa tgggggctag tgtaacagca tgcaggttga 1000
attgccaagg atgctcgcca tgccagcctt tctgtttcc tcacccctgt 1050
gctccccctgc cctaagtccc caaccctcaa cttgaaaccc cattccctta 1100
agccaggact cagaggatcc ctttgcctc tggtttacct gggactccat 1150
ccccaaaccc actaatcaca tcccactgac tgaccctctg tgatcaaaga 1200
ccctctctct ggctgaggtt ggctcttagc tcattgctgg ggtatggaaag 1250
gagaagcagt ggctttgtg ggcattgctc taacctactt ctcaagcttc 1300
cctccaaaga aactgattgg ccctggaaacc tccatcccac tcttgttatg 1350
actccacagt gtccagacta atttgtgcat gaactgaaat aaaaccatcc 1400
tacggtatcc agggAACAGA aagcaggatg caggatgggaa ggacagggaaag 1450
gcagcctggg acattaaaaa aaata 1475

<210> 134
<211> 230
<212> PRT
<213> Homo sapiens

<400> 134
Met Ala Ser Leu Gly Leu Gln Leu Val Gly Tyr Ile Leu Gly Leu
1 5 10 15
Leu Gly Leu Leu Gly Thr Leu Val Ala Met Leu Leu Pro Ser Trp
20 25 30
Lys Thr Ser Ser Tyr Val Gly Ala Ser Ile Val Thr Ala Val Gly
35 40 45
Phe Ser Lys Gly Leu Trp Met Glu Cys Ala Thr His Ser Thr Gly

50	55	60
Ile Thr Gln Cys Asp Ile Tyr Ser Thr Leu Leu Gly Leu Pro Ala		
65	70	75
Asp Ile Gln Ala Ala Gln Ala Met Met Val Thr Ser Ser Ala Ile		
80	85	90
Ser Ser Leu Ala Cys Ile Ile Ser Val Val Gly Met Arg Cys Thr		
95	100	105
Val Phe Cys Gln Glu Ser Arg Ala Lys Asp Arg Val Ala Val Ala		
110	115	120
Gly Gly Val Phe Phe Ile Leu Gly Gly Leu Leu Gly Phe Ile Pro		
125	130	135
Val Ala Trp Asn Leu His Gly Ile Leu Arg Asp Phe Tyr Ser Pro		
140	145	150
Leu Val Pro Asp Ser Met Lys Phe Glu Ile Gly Glu Ala Leu Tyr		
155	160	165
Leu Gly Ile Ile Ser Ser Leu Phe Ser Leu Ile Ala Gly Ile Ile		
170	175	180
Leu Cys Phe Ser Cys Ser Ser Gln Arg Asn Arg Ser Asn Tyr Tyr		
185	190	195
Asp Ala Tyr Gln Ala Gln Pro Leu Ala Thr Arg Ser Ser Pro Arg		
200	205	210
Pro Gly Gln Pro Pro Lys Val Lys Ser Glu Phe Asn Ser Tyr Ser		
215	220	225
Leu Thr Gly Tyr Val		
230		

<210> 135
 <211> 610
 <212> DNA
 <213> Homo sapiens

<400> 135
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 cttcgctcct gcttatgtgt cagtctgtct cctcctcttg tgtccaaggg 100
 aagtcatcgc tcccgctggc tcagaaccat ggctgtgcca gccggcaccc 150
 aggtgtggag acaagatcta caacccttg gagcagtgct gttacaatga 200
 cgccatcgtg tccctgagcg agacccgcca atgtggccc ccctgcaccc 250
 tctggccctg ctttgagctc tgctgtcttg attccttgg cctcacaaac 300
 gattttggta tgaagctgaa ggttcaggggt gtgaattccc agtgccactc 350

atctccatc tccagtaaat gtgaaagcag aagacgtttt ccctgagaag 400
acatagaaag aaaatcaact ttcactaagg catctcagaa acataggcta 450
aggtaatatg tgtaccagta gagaagcctg aggaatttac aaaatgtgc 500
agctccaagc cattgtatgg cccatgtggg agactgtatgg gacatggaga 550
atgacagtag attatcagga aataaataaa gtggttttc caatgtacac 600
acctgtaaaa 610

<210> 136
<211> 119
<212> PRT
<213> Homo sapiens

<400> 136
Met Val Pro Arg Ile Phe Ala Pro Ala Tyr Val Ser Val Cys Leu
1 5 10 15
Leu Leu Leu Cys Pro Arg Glu Val Ile Ala Pro Ala Gly Ser Glu
20 25 30
Pro Trp Leu Cys Gln Pro Ala Pro Arg Cys Gly Asp Lys Ile Tyr
35 40 45
Asn Pro Leu Glu Gln Cys Cys Tyr Asn Asp Ala Ile Val Ser Leu
50 55 60
Ser Glu Thr Arg Gln Cys Gly Pro Pro Cys Thr Phe Trp Pro Cys
65 70 75
Phe Glu Leu Cys Cys Leu Asp Ser Phe Gly Leu Thr Asn Asp Phe
80 85 90
Val Val Lys Leu Lys Val Gln Gly Val Asn Ser Gln Cys His Ser
95 100 105
Ser Pro Ile Ser Ser Lys Cys Glu Ser Arg Arg Arg Phe Pro
110 115

<210> 137
<211> 771
<212> DNA
<213> Homo sapiens

<400> 137
ctccactgca accacccaga gccatggctc cccgaggctg catcgtagct 50
gtctttgcca ttttctgcat ctccaggctc ctctgctcac acggagcccc 100
agtggccccc atgactcctt acctgtatgt gtgccagcca cacaagagat 150
gtggggacaa gttctacgac cccctgcagc actgttgcta tgatgtatgcc 200
gtcgtgccct tggccaggac ccagacgtgt ggaaactgca ctttcagagt 250

ctgcttgag cagtgtgcc cctggacctt catggtaag ctgataaacc 300
agaactgcga ctcagcccg acctcgatg acaggcttg tcgcagtgtc 350
agctaatgga acatcagggg aacgatgact cctggattct cttcctggg 400
tgggcctgga gaaagaggct ggtgttacct gagatctggg atgctgagt 450
gctgtttggg ggccagagaa acacacactc aactgcccac ttcattctgt 500
gacctgtctg aggcccaccc tgcagctgcc ctgaggaggc ccacaggtcc 550
ccttctagaa ttctggacag catgagatgc gtgtgctgat gggggcccaag 600
ggactctgaa ccctcctgat gaccctatg gccaacatca acccggcacc 650
accccaaggc tggctgggaa acccttcacc cttctgtgag attttccatc 700
atctcaagtt ctcttctatc caggagcaaa gcacaggatc ataataaatt 750
tatgtacttt ataaatgaaa a 771

<210> 138

<211> 110

<212> PRT

<213> Homo sapiens

<400> 138

Met	Ala	Pro	Arg	Gly	Cys	Ile	Val	Ala	Val	Phe	Ala	Ile	Phe	Cys
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Ile	Ser	Arg	Leu	Leu	Cys	Ser	His	Gly	Ala	Pro	Val	Ala	Pro	Met
				20				25					30	
Thr	Pro	Tyr	Leu	Met	Leu	Cys	Gln	Pro	His	Lys	Arg	Cys	Gly	Asp
				35				40				45		
Lys	Phe	Tyr	Asp	Pro	Leu	Gln	His	Cys	Cys	Tyr	Asp	Asp	Ala	Val
				50				55				60		
Val	Pro	Leu	Ala	Arg	Thr	Gln	Thr	Cys	Gly	Asn	Cys	Thr	Phe	Arg
				65				70				75		
Val	Cys	Phe	Glu	Gln	Cys	Cys	Pro	Trp	Thr	Phe	Met	Val	Lys	Leu
				80				85				90		
Ile	Asn	Gln	Asn	Cys	Asp	Ser	Ala	Arg	Thr	Ser	Asp	Asp	Arg	Leu
				95				100				105		
Cys	Arg	Ser	Val	Ser										
				110										

<210> 139

<211> 2044

<212> DNA

<213> Homo sapiens

<400> 139

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ctccccggca ccagaagttc ctctgcgcgt ccgacggcga catgggcgtc 150
cccacggccc tggaggccgg cagctggcgc tgggatccc tgctttcgc 200
tctcttcctg gctgcgtccc taggtccgtt ggcagccttc aagggtcgcca 250
cgccgtatttc cctgtatgtc tgtcccgagg ggcagaacgt caccctcacc 300
tgcaggctct tggccctgt ggacaaaggg cacgatgtga cttctacaa 350
gacgtggtac cgcaagtcga gggcggaggt gcagacctgc tcagagcgcc 400
ggcccatccg caacccacg ttccaggacc ttcacctgca ccatggaggc 450
caccaggctg ccaacaccag ccacgacctg gtcagcgcc acgggctgga 500
gtcggcctcc gaccaccatg gcaacttctc catcaccatg cgcaacctga 550
ccctgctgga tagcggcctc tactgctgcc tgggtggatgatcaggcac 600
caccactcgg agcacagggt ccatggtgcc atggagctgc aggtgcagac 650
aggcaaagat gcaccatcca actgtgtggt gtaccatcc tcctccagg 700
atagtgaaaa catcacggct gcagccctgg ctacgggtgc ctgcacatcta 750
ggaatcctct gcctccccct catcctgctc ctggcttaca agcaaaggca 800
ggcagcctcc aaccggcgtg cccaggagct ggtgcggatg gacagcaaca 850
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gatctgtcaa caggttaagt caatctgggg cttccactgc ctgcattcca 1700
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gttgccccac ccactggaga tggtgctgag ggagggtgggt ggggccttct 1850
gggaaggtga gtggagaggg gcacctgccc cccgcccctcc ccatcccc 1900
ctccccactgc tcagcgcggg ccattgcaag ggtgccacac aatgtcttgt 1950
ccaccctggg acacttctga gtatgaagcg ggatgctatt aaaaactaca 2000
tggggaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaga 2044

<210> 140
<211> 311
<212> PRT
<213> Homo sapiens

<400> 140
Met Gly Val Pro Thr Ala Leu Glu Ala Gly Ser Trp Arg Trp Gly
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Ser Leu Leu Phe Ala Leu Phe Leu Ala Ala Ser Leu Gly Pro Val
20 25 30
Ala Ala Phe Lys Val Ala Thr Pro Tyr Ser Leu Tyr Val Cys Pro
35 40 45
Glu Gly Gln Asn Val Thr Leu Thr Cys Arg Leu Leu Gly Pro Val
50 55 60
Asp Lys Gly His Asp Val Thr Phe Tyr Lys Thr Trp Tyr Arg Ser
65 70 75
Ser Arg Gly Glu Val Gln Thr Cys Ser Glu Arg Arg Pro Ile Arg
80 85 90
Asn Leu Thr Phe Gln Asp Leu His Leu His His Gly Gly His Gln
95 100 105
Ala Ala Asn Thr Ser His Asp Leu Ala Gln Arg His Gly Leu Glu
110 115 120
Ser Ala Ser Asp His His Gly Asn Phe Ser Ile Thr Met Arg Asn
125 130 135
Leu Thr Leu Leu Asp Ser Gly Leu Tyr Cys Cys Leu Val Val Glu

140	145	150
Ile Arg His His His Ser Glu His Arg Val His Gly Ala Met Glu		
155	160	165
Leu Gln Val Gln Thr Gly Lys Asp Ala Pro Ser Asn Cys Val Val		
170	175	180
Tyr Pro Ser Ser Ser Gln Asp Ser Glu Asn Ile Thr Ala Ala Ala		
185	190	195
Leu Ala Thr Gly Ala Cys Ile Val Gly Ile Leu Cys Leu Pro Leu		
200	205	210
Ile Leu Leu Leu Val Tyr Lys Gln Arg Gln Ala Ala Ser Asn Arg		
215	220	225
Arg Ala Gln Glu Leu Val Arg Met Asp Ser Asn Ile Gln Gly Ile		
230	235	240
Glu Asn Pro Gly Phe Glu Ala Ser Pro Pro Ala Gln Gly Ile Pro		
245	250	255
Glu Ala Lys Val Arg His Pro Leu Ser Tyr Val Ala Gln Arg Gln		
260	265	270
Pro Ser Glu Ser Gly Arg His Leu Leu Ser Glu Pro Ser Thr Pro		
275	280	285
Leu Ser Pro Pro Gly Pro Gly Asp Val Phe Phe Pro Ser Leu Asp		
290	295	300
Pro Val Pro Asp Ser Pro Asn Phe Glu Val Ile		
305	310	

<210> 141
 <211> 1732
 <212> DNA
 <213> Homo sapiens

<400> 141
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 ctttagacctc ctttcctgcc ctcctttctt gcccaccgct gtttcctggc 150
 ctttctccga ccccgctcta gcagcagacc tcctgggttc tgtgggttga 200
 tctgtggccc ctgtgcctcc gtgtcctttt cgtctccctt cttcccgact 250
 ccgctcccg accagcggcc tgaccctgg gaaaggatgg ttcccgaggt 300
 gagggtcctc tcctccttgc tgggactcgc gctgctctgg ttcccccctgg 350
 actcccacgc tcgagccgc ccagacatgt tctgcctttt ccatggaaag 400
 agataactccc ccggcgagag ctggcacccc tacttggagc cacaaggcct 450

gatgtactgc ctgcgctgta cctgctcaga gggcgccat gtgagttgtt 500
accgcctcca ctgtccgcct gtccactgcc cccagcctgt gacggagcca 550
cagcaatgct gtcccaagtg tgtggAACCT cacactccct ctggactccg 600
ggccccacca aagtccctgcc agcacaacgg gaccatgtac caacacggag 650
agatcttcag tgcccatgag ctgttcccct cccgcctgcc caaccagtgt 700
gtcctctgca gctgcacaga gggccagatc tactgcggcc tcacaacctg 750
ccccgaacca ggctgcccag caccctccc actgccagac tcctgctgcc 800
aagcctgcaa agatgaggca agtgagcaat cgatgaaaga ggacagtgtg 850
cagtcgctcc atggggtgag acatcctcag gatccatgtt ccagtgtgc 900
tgggagaaaag agaggcccgg gcaccccaagc ccccaactggc ctcagcgccc 950
ctctgagctt catccctcgc cacttcagac ccaagggagc aggcagcaca 1000
actgtcaaga tcgtcctgaa ggagaaacat aagaaagcct gtgtcatgg 1050
cgggaaagacg tactcccacg gggaggtgtg gcacccggcc ttccgtgcct 1100
tcggccctt gcccgcatt ctatgcaccc gtgaggatgg cccgcaggac 1150
tgccagcgtg tgacctgtcc caccgagtac ccctgcccgc accccgagaa 1200
agtggctggg aagtgtcga agattgtccc agaggacaaa gcagaccctg 1250
gccacagtga gatcagttct accaggtgtc ccaaggcacc gggccgggtc 1300
ctcgtccaca catcggtatc cccaaagccca gacaacctgc gtcgcttc 1350
ccttggAACAC gaggcctcgg acttgggtgga gatctacctc tggaaagctgg 1400
taaaagatga ggaaactgag gtcagagag gtgaagtacc tggcccaagg 1450
ccacacagcc agaatcttcc acttgactca gatcaagaaa gtcaggaagc 1500
aagacttcca gaaagaggca cagcacttcc gactgctcgc tggcccccac 1550
gaaggtcact ggaacgtctt cctagcccaag accctggagc tgaaggtcac 1600
ggccagtcca gacaaagtga ccaagacata acaaagacct aacagttgca 1650
gatatgagct gtataattgt tggttattata tattaataaa taagaagttg 1700
cattaccctc aaaaaaaaaa aaaaaaaaaa aa 1732
<210> 142
<211> 451
<212> PRT
<213> Homo sapiens
<400> 142

Met Val Pro Glu Val Arg Val Leu Ser Ser Leu Leu Gly Leu Ala
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 Leu Leu Trp Phe Pro Leu Asp Ser His Ala Arg Ala Arg Pro Asp
 20 25 30
 Met Phe Cys Leu Phe His Gly Lys Arg Tyr Ser Pro Gly Glu Ser
 35 40 45
 Trp His Pro Tyr Leu Glu Pro Gln Gly Leu Met Tyr Cys Leu Arg
 50 55 60
 Cys Thr Cys Ser Glu Gly Ala His Val Ser Cys Tyr Arg Leu His
 65 70 75
 Cys Pro Pro Val His Cys Pro Gln Pro Val Thr Glu Pro Gln Gln
 80 85 90
 Cys Cys Pro Lys Cys Val Glu Pro His Thr Pro Ser Gly Leu Arg
 95 100 105
 Ala Pro Pro Lys Ser Cys Gln His Asn Gly Thr Met Tyr Gln His
 110 115 120
 Gly Glu Ile Phe Ser Ala His Glu Leu Phe Pro Ser Arg Leu Pro
 125 130 135
 Asn Gln Cys Val Leu Cys Ser Cys Thr Glu Gly Gln Ile Tyr Cys
 140 145 150
 Gly Leu Thr Thr Cys Pro Glu Pro Gly Cys Pro Ala Pro Leu Pro
 155 160 165
 Leu Pro Asp Ser Cys Cys Gln Ala Cys Lys Asp Glu Ala Ser Glu
 170 175 180
 Gln Ser Asp Glu Glu Asp Ser Val Gln Ser Leu His Gly Val Arg
 185 190 195
 His Pro Gln Asp Pro Cys Ser Ser Asp Ala Gly Arg Lys Arg Gly
 200 205 210
 Pro Gly Thr Pro Ala Pro Thr Gly Leu Ser Ala Pro Leu Ser Phe
 215 220 225
 Ile Pro Arg His Phe Arg Pro Lys Gly Ala Gly Ser Thr Thr Val
 230 235 240
 Lys Ile Val Leu Lys Glu Lys His Lys Lys Ala Cys Val His Gly
 245 250 255
 Gly Lys Thr Tyr Ser His Gly Glu Val Trp His Pro Ala Phe Arg
 260 265 270
 Ala Phe Gly Pro Leu Pro Cys Ile Leu Cys Thr Cys Glu Asp Gly
 275 280 285
 Arg Gln Asp Cys Gln Arg Val Thr Cys Pro Thr Glu Tyr Pro Cys

290	295	300
Arg His Pro Glu Lys Val Ala Gly Lys	Cys Cys Lys Ile Cys Pro	
305	310	315
Glu Asp Lys Ala Asp Pro Gly His Ser	Glu Ile Ser Ser Thr Arg	
320	325	330
Cys Pro Lys Ala Pro Gly Arg Val Leu	Val His Thr Ser Val Ser	
335	340	345
Pro Ser Pro Asp Asn Leu Arg Arg Phe	Ala Leu Glu His Glu Ala	
350	355	360
Ser Asp Leu Val Glu Ile Tyr Leu Trp	Lys Leu Val Lys Asp Glu	
365	370	375
Glu Thr Glu Ala Gln Arg Gly Glu Val	Pro Gly Pro Arg Pro His	
380	385	390
Ser Gln Asn Leu Pro Leu Asp Ser Asp	Gln Glu Ser Gln Glu Ala	
395	400	405
Arg Leu Pro Glu Arg Gly Thr Ala Leu	Pro Thr Ala Arg Trp Pro	
410	415	420
Pro Arg Arg Ser Leu Glu Arg Leu Pro	Ser Pro Asp Pro Gly Ala	
425	430	435
Glu Gly His Gly Gln Ser Arg Gln Ser	Asp Gln Asp Ile Thr Lys	
440	445	450

Thr

<210> 143
<211> 693
<212> DNA
<213> Homo sapiens

<400> 143
ctagcctgcg ccaagggtta gtgagaccgc gcggcaacag cttgcggctg 50
cggggagctc ccgtgggcgc tccgctggct gtgcaggcgg ccatggattc 100
cttgcggaaa atgctgatct cagtcgcaat gctggcgca gggctggcg 150
tgggctacgc gctcctcggtt atcgtgaccc cggagagcgc gcggaaagcag 200
gaaatgctaa aggagatgcc actgcaggac ccaaggagca gggaggaggc 250
ggccaggacc cagcagctat tgctggccac tctgcaggag gcagcgcacca 300
cgcaggagaa cgtggcctgg aggaagaact ggatggttgg cggcgaaggc 350
ggcgccagcg ggaggtcacc gtgagaccgg acttgctcc gtgggcgcgg 400
gaccttggct tggcgcagg aatccgaggc agccttctc cttcgtggc 450

ccagcggaga gtccggaccg agataccatg ccaggactct ccggggtcct 500
gtgagctgcc gtcgggtgag cacgttccc ccaaaccctg gactgactgc 550
tttaaggtcc gcaaggcggg ccagggccga gacgcgagtc ggatgtggtg 600
aactgaaaga accaataaaa tcatgttcct ccaaaaaaaaaaaaaaaa 650
aaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaa 693

<210> 144
<211> 93
<212> PRT
<213> Homo sapiens

<400> 144
Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala Met Leu Gly
1 5 10 15
Ala Gly Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val Thr Pro
20 25 30
Gly Glu Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu Gln
35 40 45
Asp Pro Arg Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu
50 55 60
Leu Ala Thr Leu Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala
65 70 75
Trp Arg Lys Asn Trp Met Val Gly Gly Glu Gly Ala Ser Gly
80 85 90
Arg Ser Pro

<210> 145
<211> 1883
<212> DNA
<213> Homo sapiens

<400> 145
caggagagaa ggcaccgccc ccaccccgcc tccaaagcta accctcggtc 50
ttgagggaa gaggctgact gtacgttcct tctactctgg caccactctc 100
caggctgcca tggggcccaag caccctctc ctcatctgt tcctttgtc 150
atggtcggga cccctccaag gacagcagca ccaccttgc gactacatgg 200
aacgcccact agctgcttta gaggaacggc tggcccaatgc ccaggaccag 250
agtagtcggc atgctgctga gctgcggac ttcaagaaca agatgctgcc 300
actgctggag gtggcagaga aggagcggga ggcactcaga actgaggccg 350
acaccatctc cgggagagtg gatcgtctgg agcgggaggt agactatctg 400

gagacccaga acccagctct gccctgtgta gagtttgatg agaagggtac 450
tggaggccct gggaccaaag gcaagggaag aaggaatgag aagtacgata 500
tggtgacaga ctgtggctac acaatcttc aagtggatc aatgaagatt 550
ctgaagcgat ttggtgccc agctggctta tggaccaagg atccactggg 600
gcaaacagag aagatctacg tggtagatgg gacacagaat gacacagcct 650
ttgtcttccc aaggctgcgt gacttcaccc ttgccatggc tgcccgaaa 700
gcttcccggag tccgggtgcc cttccctgg gtggcacag ggcagctgg 750
atatggtggc tttctttatt ttgctcgag gcctcctgga agacctggg 800
gaggtggtga gatggagaac actttgcagc taatcaaatt ccacctggca 850
aaccgaacag tggtgacag ctcagtattc ccagcagagg ggctgatccc 900
cccctacggc ttgacagcag acacctacat cgacctggta gctgatgagg 950
aaggctttg ggctgtctat gccacccggg aggtgacag gcacttgg 1000
ctggccaagt tagatccaca gacactggac acagagcagc agtgggacac 1050
accatgtccc agagagaatg ctgaggctgc cttgtcatc tgtgggaccc 1100
tctatgtcgt ctataacacc cgtcctgcca gtcggcccg catccagtgc 1150
tcctttgatg ccagcggcac cctgacccct gaacggcag cactcccta 1200
ttttccccgc agatatggtg cccatgccag cctccgtat aaccccccgg 1250
aacggccagct ctatgcctgg gatgatggct accagattgt ctataagctg 1300
gagatgagga agaaagagga ggagggttga ggagctagcc ttgtttttg 1350
catctttctc actcccatac atttatatta tatccccact aaatttctg 1400
ttcctcattc ttcaaatgtg ggccagttgt ggctcaaatc ctctatattt 1450
ttagccaatg gcaatcaaat tcttcagct ctttggatc atacggaaact 1500
ccagatcctg agtaatcctt ttagagcccg aagagtcaaa accctcaatg 1550
ttccctcctg ctctcctgccc ccatgtcaac aaatttcagg ctaaggatgc 1600
cccgagacca gggctctaac cttgtatgct ggcaggccca gggagcaggc 1650
agcagtgttc ttcccctcag agtgacttgg ggagggagaa ataggaggag 1700
acgtccagct ctgtcctctc ttcctcactc ctcccttcag tgtcctgagg 1750
aacaggactt tctccacatt gtttggattt gcaacatggt gcattaaaaag 1800
aaaaatccac aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1850

aaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaa 1883

<210> 146

<211> 406

<212> PRT

<213> Homo sapiens

<400> 146

Met Gly Pro Ser Thr Pro Leu Leu Ile Leu Phe Leu Leu Ser Trp
1 5 10 15

Ser Gly Pro Leu Gln Gly Gln Gln His His Leu Val Glu Tyr Met
20 25 30

Glu Arg Arg Leu Ala Ala Leu Glu Glu Arg Leu Ala Gln Cys Gln
35 40 45

Asp Gln Ser Ser Arg His Ala Ala Glu Leu Arg Asp Phe Lys Asn
50 55 60

Lys Met Leu Pro Leu Leu Glu Val Ala Glu Lys Glu Arg Glu Ala
65 70 75

Leu Arg Thr Glu Ala Asp Thr Ile Ser Gly Arg Val Asp Arg Leu
80 85 90

Glu Arg Glu Val Asp Tyr Leu Glu Thr Gln Asn Pro Ala Leu Pro
95 100 105

Cys Val Glu Phe Asp Glu Lys Val Thr Gly Gly Pro Gly Thr Lys
110 115 120

Gly Lys Gly Arg Arg Asn Glu Lys Tyr Asp Met Val Thr Asp Cys
125 130 135

Gly Tyr Thr Ile Ser Gln Val Arg Ser Met Lys Ile Leu Lys Arg
140 145 150

Phe Gly Gly Pro Ala Gly Leu Trp Thr Lys Asp Pro Leu Gly Gln
155 160 165

Thr Glu Lys Ile Tyr Val Leu Asp Gly Thr Gln Asn Asp Thr Ala
170 175 180

Phe Val Phe Pro Arg Leu Arg Asp Phe Thr Leu Ala Met Ala Ala
185 190 195

Arg Lys Ala Ser Arg Val Arg Val Pro Phe Pro Trp Val Gly Thr
200 205 210

Gly Gln Leu Val Tyr Gly Gly Phe Leu Tyr Phe Ala Arg Arg Pro
215 220 225

Pro Gly Arg Pro Gly Gly Gly Glu Met Glu Asn Thr Leu Gln
230 235 240

Leu Ile Lys Phe His Leu Ala Asn Arg Thr Val Val Asp Ser Ser
245 250 255

Val Phe Pro Ala Glu Gly Leu Ile Pro Pro Tyr Gly Leu Thr Ala
260 265 270
Asp Thr Tyr Ile Asp Leu Val Ala Asp Glu Glu Gly Leu Trp Ala
275 280 285
Val Tyr Ala Thr Arg Glu Asp Asp Arg His Leu Cys Leu Ala Lys
290 295 300
Leu Asp Pro Gln Thr Leu Asp Thr Glu Gln Gln Trp Asp Thr Pro
305 310 315
Cys Pro Arg Glu Asn Ala Glu Ala Ala Phe Val Ile Cys Gly Thr
320 325 330
Leu Tyr Val Val Tyr Asn Thr Arg Pro Ala Ser Arg Ala Arg Ile
335 340 345
Gln Cys Ser Phe Asp Ala Ser Gly Thr Leu Thr Pro Glu Arg Ala
350 355 360
Ala Leu Pro Tyr Phe Pro Arg Arg Tyr Gly Ala His Ala Ser Leu
365 370 375
Arg Tyr Asn Pro Arg Glu Arg Gln Leu Tyr Ala Trp Asp Asp Gly
380 385 390
Tyr Gln Ile Val Tyr Lys Leu Glu Met Arg Lys Lys Glu Glu Glu
395 400 405

Val

<210> 147
<211> 2052
<212> DNA
<213> Homo sapiens

<400> 147
gacagctgtg tctcgatgga gtagactctc agaacagcgc agtttgcct 50
ccgctcacgc agagcctctc cgtggcttcc gcaccttgag cattaggcca 100
gttctcctct tctctcta at ccatccgtca cctctctgt catccgttcc 150
catgccgtga ggtccattca cagaacacat ccatggctct catgctcagt 200
ttggttctga gtctcccaa gctgggatca gggcagtggc aggtgtttgg 250
gccagacaag cctgtccagg ccttgggggg ggaggacgca gcattctcct 300
gtttcctgtc tcctaagacc aatgcagagg ccatggaagt gcgggttctc 350
aggggccagt tctctagcgt ggtccacctc tacagggacg ggaaggacca 400
gccatttatg cagatgccac agtatcaagg caggacaaaa ctggtaagg 450
attctattgc ggaggggcgc atctctctga ggctgaaaa cattactgtg 500

ttggatgctg gcctctatgg gtgcaggatt agttccagt cttactacca 550
gaaggccatc tgggagctac aggtgtcagc actgggctca gttcctctca 600
tttccatcac gggatatgtt gatagagaca tccagctact ctgtcagtc 650
tcgggctgg tccccggcc cacagcgaag tggaaaggc cacaaggaca 700
ggatttgc acagactcca ggacaaacag agacatgcat ggcctgttg 750
atgtggagat ctctctgacc gtccaagaga acgcgggag catatcctgt 800
tccatgcggc atgctcatct gagccgagag gtggatcca gggtacagat 850
aggagatacc ttttcgagc ctatatcgta gcacccggct accaaagtac 900
tggaaatact ctgctgtggc ctatttttg gcattgttg actgaagatt 950
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aaagcacgga caggcagaat tgagagacgc ccggaaacac gcagtggagg 1050
tgactctgga tccagagacg gtcacccga agctctgcgt ttctgatctg 1100
aaaactgtaa cccatagaaa agctccccag gaggtgcctc actctgagaa 1150
gagatttaca aggaagagtg tggtgcttc tcagagttc caagcaggga 1200
aacattactg ggaggtggac ggaggacaca ataaaaggtg gcgcgtggga 1250
gtgtgccggg atgatgtgga caggaggaag gagtacgtga ctttgtctcc 1300
cgatcatggg tactgggtcc tcagactgaa tggagaacat ttgtatttca 1350
cattaaatcc ccgttttatac agcgtttcc ccaggacccc acctacaaaa 1400
ataggggtct tcctggacta tgagtgtggg accatctcct tcttcaacat 1450
aaatgaccag tcccttattt ataccctgac atgtcggtt gaaggcttat 1500
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atagtcatct gcccagtcac ccaggaatca gagaaagagg cctcttggca 1600
aagggcctct gcaatccca agacaagcaa cagttagtcc tcctcacagg 1650
caaccacgccc cttccctcccc aggggtgaaa tgttaggatga atcacatccc 1700
acattcttct ttagggatataa taggtctct ctcccaagatc caaagtcccg 1750
cagcagccgg ccaagggtggc ttccagatga agggggactg gcctgtccac 1800
atgggagtcg ggtgtcatgg ctgcccgttag ctggggaggaa agaaggctga 1850
cattacattt agtttgctct cactccatct ggctaagtga tcttgaataa 1900
ccacctctca ggtgaagaac cgtcaggaaat tcccatctca caggctgtgg 1950

tgttagattaa gtagacaagg aatgtgaata atgcttagat cttattgtat 2000
acagagtgtt tcctaatggt ttgttcatta tattacactt tcagtaaaaa 2050
aa 2052

<210> 148
<211> 500
<212> PRT
<213> Homo sapiens

<400> 148
Met Ala Leu Met Leu Ser Leu Val Leu Ser Leu Leu Lys Leu Gly
1 5 10 15
Ser Gly Gln Trp Gln Val Phe Gly Pro Asp Lys Pro Val Gln Ala
20 25 30
Leu Val Gly Glu Asp Ala Ala Phe Ser Cys Phe Leu Ser Pro Lys
35 40 45
Thr Asn Ala Glu Ala Met Glu Val Arg Phe Phe Arg Gly Gln Phe
50 55 60
Ser Ser Val Val His Leu Tyr Arg Asp Gly Lys Asp Gln Pro Phe
65 70 75
Met Gln Met Pro Gln Tyr Gln Gly Arg Thr Lys Leu Val Lys Asp
80 85 90
Ser Ile Ala Glu Gly Arg Ile Ser Leu Arg Leu Glu Asn Ile Thr
95 100 105
Val Leu Asp Ala Gly Leu Tyr Gly Cys Arg Ile Ser Ser Gln Ser
110 115 120
Tyr Tyr Gln Lys Ala Ile Trp Glu Leu Gln Val Ser Ala Leu Gly
125 130 135
Ser Val Pro Leu Ile Ser Ile Thr Gly Tyr Val Asp Arg Asp Ile
140 145 150
Gln Leu Leu Cys Gln Ser Ser Gly Trp Phe Pro Arg Pro Thr Ala
155 160 165
Lys Trp Lys Gly Pro Gln Gly Gln Asp Leu Ser Thr Asp Ser Arg
170 175 180
Thr Asn Arg Asp Met His Gly Leu Phe Asp Val Glu Ile Ser Leu
185 190 195
Thr Val Gln Glu Asn Ala Gly Ser Ile Ser Cys Ser Met Arg His
200 205 210
Ala His Leu Ser Arg Glu Val Glu Ser Arg Val Gln Ile Gly Asp
215 220 225
Thr Phe Phe Glu Pro Ile Ser Trp His Leu Ala Thr Lys Val Leu

230	235	240
Gly Ile Leu Cys Cys	Gly Leu Phe Phe	Gly Ile Val Gly Leu Lys
245	250	255
Ile Phe Phe Ser Lys	Phe Gln Trp Lys	Ile Gln Ala Glu Leu Asp
260	265	270
Trp Arg Arg Lys His	Gly Gln Ala Glu	Leu Arg Asp Ala Arg Lys
275	280	285
His Ala Val Glu Val	Thr Leu Asp Pro	Glu Thr Ala His Pro Lys
290	295	300
Leu Cys Val Ser Asp	Leu Lys Thr Val	Thr His Arg Lys Ala Pro
305	310	315
Gln Glu Val Pro His	Ser Glu Lys Arg	Phe Thr Arg Lys Ser Val
320	325	330
Val Ala Ser Gln Ser	Phe Gln Ala Gly	Lys His Tyr Trp Glu Val
335	340	345
Asp Gly Gly His Asn	Lys Arg Trp Arg	Val Gly Val Cys Arg Asp
350	355	360
Asp Val Asp Arg Arg	Lys Glu Tyr Val	Thr Leu Ser Pro Asp His
365	370	375
Gly Tyr Trp Val Leu	Arg Leu Asn Gly	Glu His Leu Tyr Phe Thr
380	385	390
Leu Asn Pro Arg Phe	Ile Ser Val Phe	Pro Arg Thr Pro Pro Thr
395	400	405
Lys Ile Gly Val Phe	Leu Asp Tyr Glu	Cys Gly Thr Ile Ser Phe
410	415	420
Phe Asn Ile Asn Asp	Gln Ser Leu Ile	Tyr Thr Leu Thr Cys Arg
425	430	435
Phe Glu Gly Leu Leu	Arg Pro Tyr Ile	Glu Tyr Pro Ser Tyr Asn
440	445	450
Glu Gln Asn Gly Thr	Pro Ile Val Ile	Cys Pro Val Thr Gln Glu
455	460	465
Ser Glu Lys Glu Ala	Ser Trp Gln Arg	Ala Ser Ala Ile Pro Glu
470	475	480
Thr Ser Asn Ser Glu	Ser Ser Ser Gln	Ala Thr Thr Pro Phe Leu
485	490	495
Pro Arg Gly Glu Met		
500		

<210> 149
<211> 24

<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 149
gcgtggtcca cctctacagg gacg 24

<210> 150
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 150
ggaactgacc cagtgctgac acc 23

<210> 151
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 151
gcagatgcca cagtatcaag gcaggacaaa actggtaag gattc 45

<210> 152
<211> 2294
<212> DNA
<213> Homo sapiens

<400> 152
gcgatggtgc gcccggtggc ggtggcggcg gcgggtgcgg aggcttcctt 50
ggtcggattt caacgaggag aagatgactg accaaccgac tggctgaatg 100
aatgaatggc ggagccgagc gcccattgag gagcctgccc agcctggcg 150
gcctcgccct gttgtgtgc gccgcccggc cccggccgt cgcctcagcc 200
gcctcggcgg ggaatgtcac cggtggcggc gggccggcg ggcaggtgga 250
cgctcgccg ggccccgggt tgccggggcga gcccagccac cccttcccta 300
gggcgacggc tcccacggcc caggccccga ggaccgggcc cccgcgcgcc 350
accgtccacc gaccctggc tgcgacttct ccagccagt ccccgagac 400

caccctctt tggcgactg ctggaccctc ttccaccacc tttcaggcgc 450
cgctcgccccc ctcgcccggacc accccctccgg cggcggaacg cacttcgacc 500
acctctcagg cgccgaccag acccgccgccc accaccctt cgacgaccac 550
tggcccggcg ccgaccaccc ctgtagcgac caccgtaccg ggcggccacga 600
ctccccggac cccgacccccc gatctccccca gcagcagcaaa cagcagcgtc 650
ctccccaccc cacctgccac cgaggccccc tcttcgcctc ctccagagta 700
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agaccacagg gcagtgtgag tgcggccag gttatcaggg gcttcactgt 800
gaaacctgca aagagggctt ttacctaaat tacacttctg ggctctgtca 850
gccatgtgac tgtatgtccac atggagctct cagcataccg tgcaacaggt 900
aagcaacaga ggggtggaaact gaagtttatt ttatTTtagc aaggaaaaaa 950
aaaaggctgc tactctcaag gaccatactg gtttaaacaaggaggatga 1000
gggtcataga tttacaaaat attttatata cttttattct cttaactttat 1050
atgttatatt taatgtcagg atttaaaaac atctaattta ctgatTTgt 1100
tcttcaaaag cactagagtc gccaattttt ctctggata atttctgtaa 1150
atttcatggg aaaaattat tgaagaataa atctgcttc tggaaaggct 1200
ttcaggcatg aaacctgcta ggaggttag aatgttctt atgtttattta 1250
atataccatt ggagtttag gaaatttgtt gtttgggtta ttttctctc 1300
taatcaaaaat tctacatttg tttctttgga catctaaagc ttaacctggg 1350
ggtaccctaa tttatTTaac tagtggtaag tagactggtt ttactctatt 1400
taccagtaca ttttgagac caaaagttaga ttaagcagga attatctta 1450
aactattatg ttatTTggag gtaatttaat cttagtggaaat aatgtactgt 1500
tatctaagca tttgccttgt actgcactga aagtaattat tctttgaccc 1550
tatgtgaggc acttggcttt ttgtggaccc caagtcaaaa aactgaagag 1600
acagtattaa ataatgaaaaa aaataatgac aggttatact cagtgtaaacc 1650
tgggtataac ccaagatctg ctgccactta cgagctgtgt tccttggca 1700
agtaatttcc tttcactgag ctgtttctt ctcaaggTTt tggtgaagat 1750
taaatgagtt gatatatata aaatgcctag cacatgtcac tcaataaaatt 1800
ctggTTTgtt ttaatttcaa aggaatatta tggactgaaa tgagagaaca 1850

tgtttaaga acttttagct ctttgacaaa gaagtgcctt atacttagc 1900
actaaatatt ttaaatgctt tataaatgtat attatactgt tatggaatat 1950
tgtatcatat ttagtttat taaaaatgtt gaagaggctg ggcgcgggtgg 2000
ctcacgcctg taatccttagc actttggag gccaaaggcgg gtggatcact 2050
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ctactaaaaa tacaaacaaa ttagctggc gtggtggcac acacctgttag 2150
tcccagctac tcgggaggct gaggcaggag aatcggttga acccgggagg 2200
tggaggttgc agtgagctga gatcgcgcca ctgcactcca gcctggtag 2250
agagggagac tctgtcttaa aaaaaaaaaa aaaaaaaaaa aaaa 2294

<210> 153

<211> 258

<212> PRT

<213> Homo sapiens

<400> 153

Met	Arg	Ser	Leu	Pro	Ser	Leu	Gly	Gly	Leu	Ala	Leu	Leu	Cys	Cys
1				5					10				15	
Ala	Ala	Ala	Ala	Ala	Ala	Val	Ala	Ser	Ala	Ala	Ser	Ala	Gly	Asn
						20			25				30	
Val	Thr	Gly	Gly	Gly	Gly	Ala	Ala	Gly	Gln	Val	Asp	Ala	Ser	Pro
		35						40					45	
Gly	Pro	Gly	Leu	Arg	Gly	Glu	Pro	Ser	His	Pro	Phe	Pro	Arg	Ala
			50					55					60	
Thr	Ala	Pro	Thr	Ala	Gln	Ala	Pro	Arg	Thr	Gly	Pro	Pro	Arg	Ala
			65					70					75	
Thr	Val	His	Arg	Pro	Leu	Ala	Ala	Thr	Ser	Pro	Ala	Gln	Ser	Pro
			80					85					90	
Glu	Thr	Thr	Pro	Leu	Trp	Ala	Thr	Ala	Gly	Pro	Ser	Ser	Thr	Thr
			95					100					105	
Phe	Gln	Ala	Pro	Leu	Gly	Pro	Ser	Pro	Thr	Thr	Pro	Pro	Ala	Ala
			110					115					120	
Glu	Arg	Thr	Ser	Thr	Thr	Ser	Gln	Ala	Pro	Thr	Arg	Pro	Ala	Pro
			125					130					135	
Thr	Thr	Leu	Ser	Thr	Thr	Thr	Gly	Pro	Ala	Pro	Thr	Thr	Pro	Val
			140					145					150	
Ala	Thr	Thr	Val	Pro	Ala	Pro	Thr	Thr	Pro	Arg	Thr	Pro	Thr	Pro
			155					160					165	
Asp	Leu	Pro	Ser	Ser	Ser	Asn	Ser	Ser	Val	Leu	Pro	Thr	Pro	Pro

170 175 180
Ala Thr Glu Ala Pro Ser Ser Pro Pro Pro Glu Tyr Val Cys Asn
185 190 195
Cys Ser Val Val Gly Ser Leu Asn Val Asn Arg Cys Asn Gln Thr
200 205 210
Thr Gly Gln Cys Glu Cys Arg Pro Gly Tyr Gln Gly Leu His Cys
215 220 225
Glu Thr Cys Lys Glu Gly Phe Tyr Leu Asn Tyr Thr Ser Gly Leu
230 235 240
Cys Gln Pro Cys Asp Cys Ser Pro His Gly Ala Leu Ser Ile Pro
245 250 255
Cys Asn Arg

<210> 154
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 154
aactgctctg tggttggaag cctg 24

<210> 155
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 155
cagtacatg gctgacagac ccac 24

<210> 156
<211> 38
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-38
<223> Synthetic construct.

<400> 156
aggatatcag gggcttcaact gtgaaacctg caaagagg 38

<210> 157
<211> 689
<212> DNA
<213> Homo sapiens

<400> 157
tgcggcgcag tgtagacctg ggaggatggg cggcctgctg ctggctgctt 50
ttctggctt ggtctcggtg cccagggccc aggccgtgtg gttggaaaga 100
ctggaccctg agcagcttct tggccctgg tacgtgcttgcggccctc 150
ccggaaaaag ggcttgcca tggagaagga catgaagaac gtcgtggggg 200
tggtggtgac cctcactcca gaaaacaacc tgccgacgct gtcctctcag 250
cacgggctgg gaggggtgtga ccagagtgtc atggacctga taaagcgaaa 300
ctccggatgg gtgttgaga atccctcaat aggctgtgtc gagctctggg 350
tgctggccac caacttcaga gactatgccatcatcttac tcagctggag 400
ttcggggacg agcccttcaa caccgtggag ctgtacagtc tgacggagac 450
agccagccag gaggccatgg ggctttcac caagtggagc aggagcctgg 500
gcttcctgtc acagtagcag gcccagctgc agaaggaccc cacctgtgtc 550
cacaagatcc ttctgtgagt gctgcgtccc cagtagggat ggcccccaca 600
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gggcccagca ccagctcaga ataaagcgat tccacagca 689

<210> 158
<211> 163
<212> PRT
<213> Homo sapiens

<400> 158
Met Gly Gly Leu Leu Leu Ala Ala Phe Leu Ala Leu Val Ser Val
1 5 10 15
Pro Arg Ala Gln Ala Val Trp Leu Gly Arg Leu Asp Pro Glu Gln
20 25 30
Leu Leu Gly Pro Trp Tyr Val Leu Ala Val Ala Ser Arg Glu Lys
35 40 45
Gly Phe Ala Met Glu Lys Asp Met Lys Asn Val Val Gly Val Val
50 55 60
Val Thr Leu Thr Pro Glu Asn Asn Leu Arg Thr Leu Ser Ser Gln
65 70 75
His Gly Leu Gly Gly Cys Asp Gln Ser Val Met Asp Leu Ile Lys
80 85 90

Arg Asn Ser Gly Trp Val Phe Glu Asn Pro Ser Ile Gly Val Leu
 95 100 105
 Glu Leu Trp Val Leu Ala Thr Asn Phe Arg Asp Tyr Ala Ile Ile
 110 115 120
 Phe Thr Gln Leu Glu Phe Gly Asp Glu Pro Phe Asn Thr Val Glu
 125 130 135
 Leu Tyr Ser Leu Thr Glu Thr Ala Ser Gln Glu Ala Met Gly Leu
 140 145 150
 Phe Thr Lys Trp Ser Arg Ser Leu Gly Phe Leu Ser Gln
 155 160
 <210> 159
 <211> 1665
 <212> DNA
 <213> Homo sapiens
 <400> 159
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 gtaaaactgct gacgatgcag agttccgtga cggcgcagga aggccctgtgt 150
 gtccatgtgc cctgctcctt ctccctacccc tcgcattggct ggatttaccc 200
 tggcccagta gttcatggct actgggttccg ggaaggggcc aatacagacc 250
 aggatgctcc agtggccaca aacaacccaa ctcggcagtt gtgggaggag 300
 actcgggacc gattccaccc cttggggac ccacatacca agaattgcac 350
 cctgagcatc agagatgccaa gaagaagtga tgcggggaga tacttcttc 400
 gtatggagaa aggaagtata aaatggaaatt ataaacatca ccggctctct 450
 gtgaatgtga cagccttgac ccacaggccc aacatcctca tcccaggcac 500
 cctggagtcc ggctgcccccc agaatctgac ctgctctgtg ccctgggcct 550
 gtgagcagg gacacccct atgatctctt ggataggac ctccgtgtcc 600
 cccctggacc cctccaccac ccgctcctcg gtgctcaccc tcataccacca 650
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 ccagcgtgac cacgaacaag accgtccatc tcaacgtgtc ctacccgcct 750
 cagaacttga ccatgactgt cttccaagga gacggcacag tatccacagt 800
 cttggaaat ggctcatctc tgtcaactccc agagggccag tctctgcgcc 850
 tggctgtgc agttgatgca gttgacagca atccccctgc caggctgagc 900
 ctgagctgga gaggcctgac cctgtgcccc tcacagccct caaacccggg 950

ggtgctggag ctgccttggg tgcacctgag ggatgcagct gaattcacct 1000
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tggagccaca gccctggtct tcctgtcctt ctgcgtcatc ttcgtttag 1150
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caccgagtac tcggagatca agatccacag atgagaaact gcagagactc 1450
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tgattcttgt agaattaaca gccctcaacg tcatgagcta tgataacact 1550
atgaattatg tgcagagtga aaagcacaca ggcttagag tcaaagtatc 1600
tcaaacctga atccacactg tgccctccct tttttttt taactaaaag 1650
acagacaaat tccta 1665

<210> 160
<211> 463
<212> PRT
<213> Homo sapiens

<400> 160
Met Leu Leu Leu Leu Pro Leu Leu Trp Gly Arg Glu Arg Ala
1 5 10 15
Glu Gly Gln Thr Ser Lys Leu Leu Thr Met Gln Ser Ser Val Thr
20 25 30
Val Gln Glu Gly Leu Cys Val His Val Pro Cys Ser Phe Ser Tyr
35 40 45
Pro Ser His Gly Trp Ile Tyr Pro Gly Pro Val Val His Gly Tyr
50 55 60
Trp Phe Arg Glu Gly Ala Asn Thr Asp Gln Asp Ala Pro Val Ala
65 70 75
Thr Asn Asn Pro Ala Arg Ala Val Trp Glu Glu Thr Arg Asp Arg
80 85 90
Phe His Leu Leu Gly Asp Pro His Thr Lys Asn Cys Thr Leu Ser
95 100 105
Ile Arg Asp Ala Arg Arg Ser Asp Ala Gly Arg Tyr Phe Phe Arg

110	115	120
Met Glu Lys Gly Ser Ile Lys Trp Asn Tyr Lys His His Arg Leu		
125	130	135
Ser Val Asn Val Thr Ala Leu Thr His Arg Pro Asn Ile Leu Ile		
140	145	150
Pro Gly Thr Leu Glu Ser Gly Cys Pro Gln Asn Leu Thr Cys Ser		
155	160	165
Val Pro Trp Ala Cys Glu Gln Gly Thr Pro Pro Met Ile Ser Trp		
170	175	180
Ile Gly Thr Ser Val Ser Pro Leu Asp Pro Ser Thr Thr Arg Ser		
185	190	195
Ser Val Leu Thr Leu Ile Pro Gln Pro Gln Asp His Gly Thr Ser		
200	205	210
Leu Thr Cys Gln Val Thr Phe Pro Gly Ala Ser Val Thr Thr Asn		
215	220	225
Lys Thr Val His Leu Asn Val Ser Tyr Pro Pro Gln Asn Leu Thr		
230	235	240
Met Thr Val Phe Gln Gly Asp Gly Thr Val Ser Thr Val Leu Gly		
245	250	255
Asn Gly Ser Ser Leu Ser Leu Pro Glu Gly Gln Ser Leu Arg Leu		
260	265	270
Val Cys Ala Val Asp Ala Val Asp Ser Asn Pro Pro Ala Arg Leu		
275	280	285
Ser Leu Ser Trp Arg Gly Leu Thr Leu Cys Pro Ser Gln Pro Ser		
290	295	300
Asn Pro Gly Val Leu Glu Leu Pro Trp Val His Leu Arg Asp Ala		
305	310	315
Ala Glu Phe Thr Cys Arg Ala Gln Asn Pro Leu Gly Ser Gln Gln		
320	325	330
Val Tyr Leu Asn Val Ser Leu Gln Ser Lys Ala Thr Ser Gly Val		
335	340	345
Thr Gln Gly Val Val Gly Gly Ala Gly Ala Thr Ala Leu Val Phe		
350	355	360
Leu Ser Phe Cys Val Ile Phe Val Val Val Arg Ser Cys Arg Lys		
365	370	375
Lys Ser Ala Arg Pro Ala Ala Gly Val Gly Asp Thr Gly Ile Glu		
380	385	390
Asp Ala Asn Ala Val Arg Gly Ser Ala Ser Gln Gly Pro Leu Thr		
395	400	405

Glu Pro Trp Ala Glu Asp Ser Pro Pro Asp Gln Pro Pro Pro Ala
410 415 420
Ser Ala Arg Ser Ser Val Gly Glu Gly Glu Leu Gln Tyr Ala Ser
425 430 435
Leu Ser Phe Gln Met Val Lys Pro Trp Asp Ser Arg Gly Gln Glu
440 445 450
Ala Thr Asp Thr Glu Tyr Ser Glu Ile Lys Ile His Arg
455 460

<210> 161
<211> 739
<212> DNA
<213> Homo sapiens

<400> 161
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cctggaggag gaggatatca cagggacctg gtacgtgaag gccatggtgg 150
tcgataagga ctttccggag gacaggaggc ccaggaaggt gtccccagtg 200
aaggtgacag ccctggcgg tgggaagttt gaagccacgt tcaccttcat 250
gagggaggat cggtgcatcc agaagaaaat cctgatgcgg aagacggagg 300
agcctggcaa atacagcgcc tatggggca ggaagctcat gtacctgcag 350
gagctgccccca ggagggacca ctacatctt tactgcaaag accagcacca 400
tggggcctg ctccacatgg gaaagcttg ggttaggaat tctgataccca 450
accgggaggc cctggaagaa tttaagaaat tggtgcaagc caagggactc 500
tcggaggagg acatttcac gcccctgcag acggaaagct gcgttcccgaa 550
acactaggca gccccgggt ctgcacccctt agagcccacc ctaccaccag 600
acacagagcc cggaccaccc ggacctaccc tccagccatg accctccct 650
gctcccaccc acctgactcc aaataaaagtc cttttcccc aaaaaaaaaa 700
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 739

<210> 162
<211> 170
<212> PRT
<213> Homo sapiens

<400> 162
Met Lys Thr Leu Phe Leu Gly Val Thr Leu Gly Leu Ala Ala Ala
1 5 10 15
Leu Ser Phe Thr Leu Glu Glu Asp Ile Thr Gly Thr Trp Tyr